

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLGAQIM*GQEFET
11562	25463	A	11662	142	437	GQRVQIFFFFWKRFPFFAQQGTEGAQFR LIKPSPSGLKEIPPPNPPRKGE*RDGPP FRGDFVFLRKNGVPPCGQGGSKPPAPGE PPFFTTPRGENNRRG
11563	25464	A	11663	120	353	QALQVMLKHVNNFFFLFFLFWKQSFVPL PRLECNGATSVHCNLCPLG*RNFPASAQ EFRIAGSYDHAICPPASGKGE
11564	25465	A	11664	1	404	NTWSDLIISYFHPRPSAFFLRQGLALSP RLEYRGTTIGHYSLDLWGSSDSPASISR VAGTTYRCM*FQLLGRLLRRENLSPRGR GCSDP*LCPYTPAWVTERDPVSKKKLRG GGENSLSSQTMV
11565	25466	A	11665	493	3	NIWIPDVLPGHARQ*LGSPGKLSAGF* PLQFPQTLSSARAPPFCRLRLQVRNTVG FLPSPHTSRPSHCLPACPLPSRTQPWVP VKPGPTACRGFLQHPPTPGSPSP*SFQG SSWWDTDLRALECLLRILGRNCSVFVT TQGQLSHEGMNKEFLLTCAKKKK
11566	25467	A	11666	3	401	CMERAVTVLLPGSATQSPVYAPRALAR LWLTAAMMISGFIADYE*SSRCSSACP AGDSLSYHSPADSFSIMGSPVGAQDFC ADLGVSRANFIPTDDMTSPDLQWLQVQ PALVYSVGPSETIAPHPLGVP
11567	25468	A	11667	1	446	LSCAKPPQRLRHGIIKIFNVFEETRAN KHLGLVSKLKPRGFPAFLSVSSFGQKK HVPQWLQSHSHILVISLDDFFFFFEK KPPFFPPGGRERDQTFN*TPPRGG*RE SPPFFPSRGGGTQGWAPHCP I IFRFQKK GVFPLRAR
11568	25469	A	11668	18	403	DPLQRPQYRGCLRSVGC DLQSPTPRGPS GRWPNPAQARGPGEAQAWAWPGGPREA FSGQGRPPPLGLPHRRKGAGPPGPMGP *HEGQGS*GASCRGGLACTAFPAASSP PIFGGLTPPNLNFPEE
11569	25470	A	11669	157	1	PRPQGFVVFVFFFFEMQFRLECSGAISA H*NLHFLGSSNSPASASHVYAPLY
11570	25471	A	11670	396	7	EKVCQARDKSACEGHSCADARSCLHLRV DQGGQHGSHGACPGRRLRGPDTHRQSCY QCRCNRPDLRQPGRAGTP*CAEAAAEP DAAVHPGQPAPARLPALPGRGLPLPH PGGSQRVYCVRCIGSKLR
11571	25472	A	11671	209	3	DDLGTHRPGKSQVRVTPREAGENPSAVL PCYLHLVPFV*EDEVKPEDSIPDMPGNE YAREFLAHAPLY
11572	25473	A	11672	270	101	LSLNRWILGAYIIFFETESHVAQAGVR *HNLGLLQSLPPGSRRLPAFKVAFLEFIG
11573	25474	A	11673	421	592	SSCTPGVIKIPCVRSNHMKLPGPMVA HTCNPSTLGGQGGRTWSE*FKTRLGNM A
11574	25475	A	11674	176	6	LTFVYMPFCFALSSIMTYGLAM*FHFH SMTLFIIGVLSVALAIYQ*WLDVSRVSV
11575	25476	A	11675	1	418	NTVCVCVCVCVCVCVERKAGHRLTDSFP IQAGPGAQARTLCLRESTGGALSSGLPA SRYQDPGRGALPHCVWTPRGWNWRLNY PPARSPSREAVCYFRQTLKKWRSRPGQG GRILRVIRTASTFRDTS*TESACLGARP CLDGK*VCESVPCFSLHHTHTHTHTHT

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						HCI
11576	25477	A	11676	305	698	SFMGRSPRKIDQFCNSRNMVHGSVTFRD VAIDFSQEEWECLQPDQRTLYRDVMLEN YSHLISLGSSISKPDVITLLEQKEPWW VVSKESTRWYPGK*E*SRQGEAIIIVPDS PCAQRGVTPLRGLENFLQ
11577	25478	A	11677	107	397	GGDGRETLRAPADDGCI*QERAETPLAI SCPRSSSTCRGRARRYDGCRTDGHQLI QRGQQQESSRRTAQPGSSKLCRGPGGHR PSLGTGVGHGCSL
11578	25479	A	11678	514	554	RAKPTPP*GGGEGQNFGLLKPPVSGLP LACPTPPKRWKPKPPPPAPPHLFF**K RGLIF*PGEVFNLRNWKLPSPPPQRGGN KGRNQPPPRGTFMF
11579	25480	A	11679	266	3	GPPLFLGLKN*TFFSPTKV*IFFSQVFS SFPQGLKGVREIFFFFFFFF*DRLECNGT ISAHCNLRLPGSSDSQASAGTTGVCHYT RMY
11580	25481	A	11680	1	408	NTCALRHRDHFSFWSDGKTEGEERIVQ ENWLISWNNFSPETLLTLSCPLGKEGM PGEDGTAGAGKVPGEDKIPG*DGTAGED GTEDENGTTGEDETAGVGKTPGAGGTTG EDDTESEDGTTGEDETAKGGTAG
11581	25482	A	11681	244	420	KDSESTKAYIRDNISSTKKKSWPGAGA HPCNPSTLEGKGG*IT*SQEFETSLANM VKL
11582	25483	A	11682	294	443	QMNTCTHIQPAYVH*EKYFRPSAMAHAL NPSTLGGRGGWIT*SQEFQTRP
11583	25484	A	11683	346	1	YNTNQFTLRGTQASVYTCLTALIVLKL NQPYTLASVLLNAGNQPFHAFSPPSLH PDAFHSKIMSHIIILLGFIPFLPASQS LTLSPSLERSGTISAQCNLCPLGSSNSP ISA
11584	25485	A	11684	140	423	SSHQASSPPTTASHSMKISVAAIPFLL ITITLGTKTESSSRGPYHPSECCFTYTT YKIPAQRMIDYYETNSQCFKPGIVFITK RGHSRWTNPK
11585	25486	A	11685	163	3	TKIPCNRLKFGPPSCCGFFFLPFPFF FEETLSRSVAQAGLOWRDLGSLAL
11586	25487	A	11686	179	1	PIVFLGMLFVAFARFPFESVTKPPNFF FFFEMESCSVAQAGVQWRDLGSLQARPP RST
11587	25488	A	11687	192	1	EQGFDGHLASWISLKD TAKWNGDELCS YYQSCCTDYTAECKPQVTRGDVFTMPED EYTVYDDG
11588	25489	A	11688	89	3	SGGYCCCLCCRSRYSCCCRLREGPTK
11589	25490	A	11689	168	2	QDRLQPHESKRKLGAPQLRRSESDTPS VVNFQSTESQLMSKGEDTKDDSKETV
11590	25491	A	11690	301	397	HFVFSLV TGMNPLSPYLNVDPRYLQVR LRFY
11591	25492	A	11691	18	421	TKALQITCYLHSTMSEESDGKLIEDSLI QLRCHFTWKLLEAPEIPDENRIWEEI QFLDTKYNVGIHNLAYVKHLKGQNEEA LVSLKKAEDLIQKEHANQADIRSLWTG NFAWVYYHMGRLAEAQTYLDKV
11592	25493	A	11692	188	3	PLQGGKGFKAERGQKKGFLRGGVASRP RPPFGPSLFFFFFFETDSHSAQDGVQW CDLGS

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11593	25494	A	11693	24	391	APRADAMGHFTEEDMATITSLWGQGNVE DAGGETLGRLLDVYPWTQRFFDSFGNLS SASAIMGNPKVKKAHGKKGLTSLGDAIQH LDDLKGTFSQLSELHCDKLHVDPENFKP LGNGLQTALQ
11594	25495	A	11694	138	425	NSGVKAAFQLNPGNPNEGKPGPGFKTH PGQLGETHFLKIHYSGLVGKPWESQL LGNLNRNHWTPERGGPRDLRHCHGIQP WATNGNFVLKKK
11595	25496	A	11695	158	838	CGTVHSCDAGQRQATAPSHPCDHGNQO PILYRVLCCQLFWILCFVFSHIMSTKC PSVSPVSGEMKKRKAITLEMLKIIAQH EGGKPVMAIARELGLWQSTISTILRDKK QISDAAKSSASVKSTVITKKRAGPIDDM EKLVMWMEDQIQKRIPLSLMIQAKAR SLFNMLKDRASDPTTYTQMFKASHGWFQR FKRRHNFHNVKITGEAARAGNEGAIAFK EQL
11596	25497	A	11696	834	1431	SSACQGSQGWPPRQFWMMWGSRRAPS VTHRTGERCSTSGSAPLPLLLSSLCSSL PRSWEHSTLRQPPHPPLLPGLPPGRE AQRLSGAGHGPGRFAAASYIPDTQADR KQQQHHPGPDQHVGHREGLALEDAAATHL GLVAALSCWLLGRAEAGYQVPHGHDHPK DQHPQADGGQRIVRAIGLGLGHHVSGRR ARP
11597	25498	A	11697	143	1	ISKERGASRFSGPWVFFFFFFLESRSVAQ AGVQWCNLGSLQAPPPGFT
11598	25499	A	11698	58	459	KGKEEKVKRKEAEQNFSPYAQDKQERIK GNENDEKTKQKQETIIDIELFKGLDETG ENMDSTLRTPTPEPLENNKQILVLGLDG AGKTSVLHSLASNRVQHSVAPTLGFHAV CINTEYSHMEFLEIGGSKPFRS
11599	25500	A	11699	215	1	GTTKALWAGGGGFFPYLPMPGLGPICG GVGKGSPLGCPIFFFFFFFFETESCSVA RLDAQWPDLSLQSP
11600	25501	A	11700	300	420	KPKILFGNVFAAPHMENLKRGETVAKE ISEAMKVKAMC
11601	25502	A	11701	351	466	RIKNADLSQAQWFTPVIPALWEAKVGRS LEVRSSRPVW
11602	25503	A	11702	172	400	SNRLRNKIQGVFLNDSSISPFILRKQSI GQAWWLTPVIPALWKAASGSPMDSTT LLPSSSQVPSLVKMEKLNYS
11603	25504	A	11703	284	408	ASVFSSFFVCLFVFEMESRSFAQAGVL WRDLGSLQAPPPG
11604	25505	A	11704	20	447	LPGADYGGGHLRLFLHLLASAAWVPD ESQVTLSAICVLSTVLIMEFPDLGKHC SEKTCQQLDFLPVKCDACKQDFCKDHF YAAHKCPFAFQKDVHVPVCLCNTPIPV KKGQIPDVVVGDHIDRCDSDHPGKKKEK IFA
11605	25506	A	11705	1	455	HS CSLQFTPTAWDCTGSVSSEQGERPAA AMKICSLTLLSFLLLAAQVLLVEGKKKV KNGLHSKVRSEQKDTLGNTQIKQKSRPG NKGKFVTKDQANCRWAATEQEEGISLKD ECTQLDHEFSCVFAGNPTSCPKAQDERV YWKQVARKLRS
11606	25507	A	11706	1	428	DAEADKMAAAVRGGRSGSGGCSGAGG

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						ASNCGTGSGRSGLLDKWKIDDKPVKIDKWDGSAVKNLSLDDSAKKVLLKYYKVENFGLIDGRLTICTISCFFAIVALIWDYMHPFPESKPVLALCVISYFVMMGILTYTSYRE
11607	25508	A	11707	1	422	RSQARSSAAAAARASVPLRGSPGPSAIMPMFIVNTNVPRASVPDGFSELTOQLAQATGKPPQYIAEHVVPDQLMAFGGSSEPSALCSLHSGKIGGAQNRYSKLLSGLLAERLRISPRVYINYYDMNAANVGWNNST
11608	25509	A	11709	88	423	AADAMKQAEEMAGAFMRLAYQELQIDRLKEDKMLNLNLEGNKREHAERLGMGLVSRSSVSHSVLSEMLVIEHETPVSAKSSRSQDLDFDDVGTFCSGPSKYTDNPFSLWESIG
11609	25510	A	11710	393	130	NPSATAQSFHLAARKLSTLDRPGSQAPQKMPSPKPGVVLPASTNAVPTPLAEATPSKAHPAISLLSTEELFKAVPSPASSCSFLHV
11610	25511	A	11711	331	440	KIFFLNFLISRWWCAPLVLATWEAEVGESLYPRRS
11611	25512	A	11712	122	478	SGLCPQQPPRANSCPPSSMASCAEPSEPSAPLPAGVPPLEDFEVLGDVEDAQGEEEDEEEEEEDDLSELPLEDMGQPPAEAEAEQPGALAREFLAAMEPEPGPSVPKEWLDILGNGL
11612	25513	A	11713	102	2	TNLGNPRRPPPPFFFTETVSLLAQAGVQWCDLGS
11613	25514	A	11714	126	2	FFAPFLKIFFFFFFFSEMESCSSLQAGVQWHDLGSLQNEGSQ
11614	25515	A	11715	178	449	LSGGNLFGTIILLYCAIIGGKLLGLIKLPTLPPPLPSLLGMLLAGILITNIPVINDNVQIMHRWSYSLRSIALAILVRAGLVLESKALEK
11615	25516	A	11716	48	417	GSGGNHNSVCCDTMEGGGGSGDKTTGVLAGFFGAGEAGYSHADLAGVPLTGMNPLSPYLNVDPRYLVDQDTEFLPTGANKTWGRFELAFFTIGGCCMTGAAGAMNGLRLGLKETQNMASKP
11616	25517	A	11717	103	2	PKSPTQWLMAVIPALWEAKAGGSRESRSSRPAL
11617	25518	A	11718	1	413	WPSGQVLVGCLSFSLYCWKRSLKRNKPGFEVLLKIFLKNHPRCHTNRMQLTATPVSALEDEPAHIRATGLIPFQMVSFQASLEDENGDMFYSAHYRANFAEADLNHAASLGGDYLGDLALRLCTLEPVFPQSY
11618	25519	A	11720	116	462	AGMLPAVGSVDEEEDPAEEDCPELVPIETTQSEBEEKSGLGAKIPVTIITGYLGAGKTTLNLYILTEQHSKRVAVILNESGEGSALEKSLAVSQGGELYEEWLELRNGCLCCSVK
11619	25520	A	11721	167	407	EIYSLTRFIEVKMSKKISGGTVVEMLGD EMTRI RETLKEKLIFPYVESHLHSYDLGIENRDATNDQATKDALEAFNKPYP
11620	25521	A	11722	254	423	NQLSSIMAMFKKIKSFVVFNDEPKVYGSGEKVAGRVIVEVCEVTRVKAVRILACG
11621	25522	A	11723	3	424	VSCDTMEGGGGSGDKTTGGLAGFFGAGGAGYSHADLAGVPLTGMNPLCPYLNVDPRYLEQDTEFLPTGANKTRGKFELALFT



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						IGRCCMTGAAGFAMNGLRVGLKETQNM WSKPRNVPIIDMVTROGALWANTLGALA
11622	25523	A	11724	2	343	AFGTMKWVTLVSVLFLSSAYSRGVFR DAHKSEVAHRFKDLGEENFKALVMIAFA QDLQQCPFEDDAFSTSEVPEFATTCQDD DHFEDRCRRVHTLVVVQLCTPATLLET DY
11623	25524	A	11725	1	359	HAFGTMKWVTVISLVFLFNSAYSRGVFR RDAHKSEVAHRFKDLGEENFKALVLI AF AHYLHQCPFEDHVKLVDVTEFAKT CDA DESAENCCKSLHTLFGDKLCTVATL QET Y GEMADC
11624	25525	A	11726	1	349	GAMSDRKFSAPRHGSLGFLPRKRSIR HR GKAKSFPKDDPSKPGHLTGFLGYKAG MT HIVREVYRPGSKANTNEVAEAVTIVET P PMEVADIAGYMETPRGLRTFNTAF AEHM SDEC
11625	25526	A	11727	81	349	TKGSVVSCCVCLCVCLCTWSHL CRLVTW LPDMPDDVLWLQWVTSQVFTRVLM CLLP ASRSQMPVSSQASPTCEQDWPCWTP C SPEGC
11626	25527	A	11728	264	388	QADPKDIMKFPGLNQLRSLFLEKAIT REAQMVKVNVKRM
11627	25528	A	11729	2	471	PGCSASWSKRGSGPMDLSSMAAAGSV KA ALQVAEVLAEIVSCCVGPEGRQVLCT KP TGEVLLSRNGGRLLLEALHLEHPI ARMIV DCVSSHLKKTGDGAKTFIIFLCHLL RGL HAITDREKPLMCENIQTHGRHWKNC SR WKFISQALLTFQTQIL
11628	25529	A	11730	160	377	LQGFGRPSVYHAAIVIFLEFFAWGL LTT PMLTVSIAELGLCFVRERDKFLGTY HCV CLDTCGLGVALDSDLKQ
11629	25530	A	11731	45	438	KLQQRKEATVTKECKSKSRKVGSPDR F RSPQKRSGRQDCFTLFCFWKVL DKNME LISPTVIIILGCLALFLLQKKNLRRP P CIKGWIPWIGVGFEGKAPLEFIEKARI KVCGRGRRGLQRRQCFLF
11630	25531	A	11732	169	292	DSILLVNLACSAVISAHCNLR LPGSSDS PASASRAAGGAHL
11631	25532	A	11733	473	600	KFWEKRTEGRGKSKSKNSETGEIV SISA LSTTEVAMHTSTSS
11632	25533	A	11734	19	349	APSPDAMGHFTEEDKATITSLWGT VNVE DAGGETLGRLLGDYPWTQRF FDSFGNLT SASAIMGNPKVKAHGTVLTS LGDAIKH LDDLKGTFAQLSELHCDKLLVDP ENF
11633	25534	A	11735	234	359	FYHLKSFTVSSVQSRWLTPV IPALWEAE AGGSPPEVKSSRPAS
11634	25535	A	11736	15	372	KLPLKALTGEEKTHINIDIIGHV HSVKS TTTGHLYKSRGIDERTIEIFEKEA AEM KGSGFKYACILDKKAERERGITID ISM RKFETSKYYVTIIDAPGHRDFIKDM TTG TSHADCA
11635	25536	A	11737	1	357	IWKAAAMASPAGSWARPPRPMREP QTLAM PTNAEDQKLKLERLMKSPDLAVT IPEK MSEWSGPPPEFDRDVMGSRAGAAS GEF HVYRLRRREYQRQDYMDAMAEKR ILDA EFQRRLE
11636	25537	A	11738	24	335	APNANAMGHYTEEDKATITSPW GKGNVE

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						DAGGKTLGRLLDVYPWTHRFFDFRGNLS SDSAIMGNPDKAHGQKVLTSLGDATAKH LDDLKGTFAQLSELHCDKLH
11637	25538	A	11739	141	335	MQFLPCIPILKSLEKSVASHSQTVHSDI ISTVEFNHTGELLSTGDKGGRVVIQRE QESKNQVHR
11638	25539	A	11740	7	337	APSPDAMGHFAEDKATITSLWCKVNVE DAGGETLGRLLAVYPWTQRFDSFGNLT SDSAIMGNRKVNAGHTKVLTSLGDAIKH LDDLKGTFAQLTELHCDKLHVDPENF
11639	25540	A	11741	182	360	SRHSISPPVNQIQLGASVTEELTVVTKT ARVSRAQWLMFVIPALWEAEAGESPEVR NSR
11640	25541	A	11742	174	1	HFSDSLFLVCVRQDLTLLPRLECSLIT AHCSSLHLGSGDPPTAASWVSGNTGVHY HA
11641	25542	A	11743	75	218	KTILGRAQWMTVIPALWEAKVGRSPVS ASQSAWDYRREPPCPSCTI
11642	25543	A	11744	168	2	LAPLWSLGPVLGGVGQSGPGGFFFFF FFFFETESCSVARLECSGPILAHCSLR
11643	25544	A	11745	83	2	REQRFLLPFVQLCPAPRGGVYRGRQAS
11644	25545	A	11746	156	3	FHSGSGRVENPSFFFSFFETGSCSVTQD GECTGATLAHCDLCLGSSNSS
11645	25546	A	11747	244	330	KDRAQWVTPVIPALWAAKAGRSLEVRSS R
11646	25547	A	11748	201	1	TSQPLIRITLSTFFFFSRDGGTLMLPRL DPELPGSSNPPSCSASRVDTTGMCHHT RLIFFSQTDKK
11647	25548	A	11749	262	3	VYTSLTTPPPISVNLITQVSPRSVSYEQN ILCLLFVITYFTCTFFVCLFVCLFVCFK MESCSVAQAGVRWRDLGLLQAPPGFTY TT
11648	25549	A	11750	225	3	PIINFSVPQFLHLYNGIIESTPPSCCI LKCQSLGQAQWFTPVITLWEAEAGRSL EAWTLKTI LANMAKPHL
11649	25550	A	11751	185	2	VSTPFNSFPSPWDLVFLKGFFFFFFFFF FFETEFCSPLERNGAPLAHCNLRRLPR SSNSP
11650	25551	A	11752	261	336	DRVSLWSPRLECNCAISSHCNLRLP
11651	25552	A	11753	282	381	TDLLYKKKCGLGAVAHAYNPSALGGQGG RITCS
11652	25553	A	11754	202	45	NERKVKLQWALILPLPFLNGQLKSRFQ KKKKKKKKKKKEKRRKKTLVVIC
11653	25554	A	11755	293	357	LTPVIPALWEAEVGGSPVRS
11654	25555	A	11756	264	1	TLPIINVCCDHSTGSPSLISLPLLSLPYS LRHNNIEIRLINNPTTACKYSCLKKSHK SLTLDQKLEMIKLGEEGLLKAQIGQLG LLHQ
11655	25556	A	11757	126	1	ILPGFLKELKIELPFNPAILPLGIYPKE KKLLYQKDTCTHMF
11656	25557	A	11758	399	226	IEKGTGRVWLTTPMIPALSEAKAGGSPE VRSPRPACIGLLKFWYYRCEPQHPARLS EI
11657	25558	A	11759	235	380	DTTVLKLGLITLQWASKCSSERKSRTS LTLTQKLEMVKLSEEGMSKGD
11658	25559	A	11760	249	357	NRASGQTCPTPIMPALWEVEAGGSLEP RSLRLTWA

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11659	25560	A	11761	168	372	KLHCLLCFYLSSEFFVFCFLETSLSLVAQSKCSGTVITHCSLKLCSDDPATSDSRVAETTGTGYHAGL
11660	25561	A	11762	303	377	QFAGCRWLMPVIPALWEAKADGSPE
11661	25562	A	11763	135	1	ATTPGLFFIFYFFETESHSAQAGVQCMISVHCNLCCLPGSSDSPV
11662	25563	A	11764	219	2	KLRSSQLSEPEVRPDSTLSMLMHARAHTHTHTPHLFLPHPCSRPHTSTPTCMPIVTHSPIYLKFKHSHTYIL
11663	25564	A	11765	102	1	NRPINNPTMASMCSSERKSHKSLTLNQKLEMIKL
11664	25565	A	11766	245	3	PGEPEEDQLVKFRPSLLWVFMFLFLRRSLALSPRLCESGVECSGVISAHCNLCITGFKQFSCSLSLSGWDYRHVPPCPS
11665	25566	A	11767	350	97	GSVPASPQVTRPTLMTSLADKWFSLCLTSLRVNFGVALILSGSHSVSQDTLDDLTLFSTHLGLPKCDYKRVPPCSAQFLVTF
11666	25567	A	11768	188	391	LGSVAGDLLCFFGGVIFPCSFMFMSLCYYLYIWNVCVFLFFKTEPHFVTHSGVHWCDGLLQPPPN
11667	25568	A	11769	131	2	YTLYIPNKSPIENIQLSWAQWLVPVIPA LCGAETGELEPRSS
11668	25569	A	11770	165	1	VLIPLIHLCIYIYIYTYICVYIYTRYIYTHICITHVYIHIYVYIHTYIYTYMYTY
11669	25570	A	11771	72	1	ILLFFFFFFEAESCSVAQAGMQWCN
11670	25571	A	11772	121	3	TSEVLFCEFEFCSCCCPGLECNGAILAHCNLRPLPGSSD
11671	25572	A	11773	152	3	HVCLNLTLPPLFEKNIFSLCVCVCVCVCVCVLCCKKKCKEKFYFERTF
11672	25573	A	11774	190	2	GFSPRQRGAPRVPPPLAGFPPIFFFFF FEMWHSVAPAGVQWCNHSALALTSPDSGDPP
11673	25574	A	11775	287	1	GAHRRKLFITPGESLRDKQIAGFEHRRGGEKKKTLFYKKKKKKKKRKEKKGKMKMLPKCNYTMKNHQVPYSIRPTRECADLRVYFIKFQILKY
11674	25575	A	11776	121	3	KCASRDLSKFFFFFFFLETESRSVAQAGVQWCDLGSQAL
11675	25576	A	11777	142	1	EKTLHVRNTIHNSEGLVIKIHGR LGVVAHACNPSTLGGRGGQITRS
11676	25577	A	11778	179	3	SHQVPVPGTLDLPRGPQKLQSTSEAESEASMSSEASSELVPPLEAGAAPYREEEAAKK
11677	25578	A	11779	147	6	KTPGLKKNSNFFFFFFFETRSHSIARAGVRGCDLSSIQPPPLGLK
11678	25579	A	11780	184	3	GFGFYIIPNYRLFFFSLLIGPFFFLIFFETEPCSVARLECSGVISAHCNIRLLGSCDSPA
11679	25580	A	11781	120	319	VKSLAKFLVNYQLHRQTCSGQAGRGALRQRFGPRQVDHLRPGVRDQPGQHGETPSLLEVRKLSSG
11680	25581	A	11782	91	3	YICLSLIYTHTHTHTHTHTHTHIYIVCV
11681	25582	A	11783	221	332	SRLGMVDHPRSGVRDHPGQHGETPSLLKIQKLARRSG
11682	25583	A	11784	243	379	LKYSVPKCKPWPPTWDHTRNPSTLGGQGGWITLDQKFETSLAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11683	25584	A	11785	327	5	GRVDSQPIYPKNPPGSFPKIYPGSFKTL FPYLQSRHSFSIPRSKLARFHQAKPLFC SKPSQSLSPHSELKKKDLSQLARWLTPVI RALWESKAGRSPEVRSRPTWPT
11684	25585	A	11786	245	359	FKGMDRLRSGVRDQPGQHSKTPSVLKIQ KLAGHGMRL
11685	25586	A	11787	356	67	RDIASITARLRYDRGVGITRLEVLKSD EYTKGSVLDFSRETEPIGYIYIYIYIYI YIYIYILHSLPLNHMEISLGHPPLSNNKF VQNFDSPKLSYH
11686	25587	A	11788	103	3	KYIIPVCIFFFPETESCSVTQSGVQWCE LRRRG
11687	25588	A	11789	136	1	VHQFTIRILNYYYYYFFETESYSVTQAG VRWCNLGSLQPLPPGFK
11688	25589	A	11790	291	163	SLLLLPRLCNCSTISAHNPRLLGSSDS PASGRSLEPRSSKLQ
11689	25590	A	11791	107	2	IFMYVFFETESRSVAQAGVQWRYLGSVQ APPSGFS
11690	25591	A	11792	329	3	KNPRNIIGKSRGPYITNFPDGKPKNSS PRGNDLSINKNWAQAFQPRGQKLFPPK KKKKKETQSR SIPRLCNGPTIAQCNLK LLASSNPPTSASHSAATISMSHSG
11691	25592	A	11793	213	3	ISPWLFLLLQATLFRSQYGPFPFPLSL PYLFPFKQKLGSGFFFLFFFKTESRF LARLECSGIITAQ
11692	25593	A	11794	1	400	KRAAPQPAPEQRDLKKKKKKPPLAPSSL FRFWEKLLPSFQFRQPRGPFGLTRGVSF AFHRRRFWQYGNMGEKQTWGNPGSSNP PPGTAGSLSGNRGPWGCKIADRFWLYA RDSFGHSRGLKGSQCAHLGK
11693	25594	A	11795	3	769	RKEQTRNARAEVLRQAKANFEKEERRKE LKRLRGEDTWMLPDVNERIEQFSQEHVS KKKKKKDKHKKAKKEKKKKSKKQKYEK NNESSDSSSSSEDEWVEAVPSQTPDKEK AWKVDEKSGKDDTQIIRDEWMTVDPM SVKTVSSSSLKAEKETMRKIEQEKQAL EQSMEIFQSKLEDAEKAASTKEDYRRER WRKPTYSDKAQNCQESRESDLVKYGFCS RDRYATDTAKNSNNEKFIGDEKDKRPG SLE
11694	25595	A	11796	110	13	HTHTHTHTHKHTHTHTHTHKDRSGKIKC VPTV
11695	25596	A	11797	184	2	SEIFGKFHVFIYILT VHFMPPTQVYVERD VLGQEQLLTPVIPALWEAKAGRSPEVRS SRPA
11696	25597	A	11798	83	387	GERRRRRRRLWAPLQKKKKKKKKKKKK KKKKKKKKKKGGAPLKKPPGGPHFSGG RQKNIPPLKGGELKRAPAGDFKNPGRGK IARGGFFEKNLSWGGEK
11697	25598	A	11799	153	2	IPWEDTVYSGYPQFLFSHSFFYFYFFE TGSCSLTQTGVQWCNHSGLQPR
11698	25599	A	11800	93	3	VWGRAWWLTSVISALWEAKVGESPEVRS S
11699	25600	A	11801	115	1	NPLFFFFFFFEMESCSVAQAGVQWCNLG SLQPLPRFK
11700	25601	A	11802	295	137	RCFIFILFINKLYFVYLFYFFEMESHT VAQAGVQWRDLGSLQAPPPNKLYF
11701	25602	A	11803	287	1	MGPAPFKGTCCGGFQDFRFXNLEISAGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						THSPLLAQNFRVGA VPSPRYS PRFGSKG GGGFFFFFFFFFETESHVAQQAGVQWCD LGSLQALPPGF
11702	25603	A	11804	202	3	WSVCCFKQGLGLSPRLECNGAPGFKQSF PLSLLSNWGYRGPPRLNFFFFFFFFEMES CSLAQAGVQR
11703	25604	A	11805	3	315	FMLLILTLFLLRNDRLVQCDVRSSVVC GFLLGWSVILYPLMAAFMPTMWIFLFI FSMLFFYVFFLFLFLFLFLYSPLEFCF FFCFYLFRRFFFFLIFFSSP
11704	25605	A	11806	126	3	KRGFFFFFFFFFETESRSFAQAGVQWC DLGSLQALPPGV
11705	25606	A	11807	130	2	QSIKMTCSLYFFIKKNVAWWLTPVPA LWEAGAGGSHEPKS
11706	25607	A	11808	149	1	GGKKAILFFFFSLSPRLECSGAIPTHCK LCLPGSRHSPASAFRVVGTAG
11707	25608	A	11809	258	3	KYYYQGNRQIKFVNAKSNKNLPSYSQKA SWFSSRNIRMMGQHQPMLDNPSTFIKK LGQAWWLRPVTIPALWEAEAGGSLEBSRL
11708	25609	A	11810	153	285	CASPIRSHQKLNKNGVQWLMPTVPVPW EAETGGSLQLRSSRLA
11709	25610	A	11811	160	3	NHLFLLLNRYKSI FIGRVQWLMPVSSAF WEAKAGRSFEPRSSRPAGQHGTKL
11710	25611	A	11812	89	2	AAAAAAAAETVSCSVAQGGVQLCHLHSLQL N
11711	25612	A	11813	254	336	LLGQPQWLTPVIPALWEAEAGRPSEVR
11712	25613	A	11814	108	2	CVGVLGFFVCLFFETESCSVAQAGMQWH DLGSLH
11713	25614	A	11815	166	289	SHSGWNAVWRDGS LQPLTPGFKRFPCLR VPSSWDHKCAPPC
11714	25615	A	11816	192	2	DKDPGKVTRPFLLLCIFLYFICLFLRRT LAVSPRLEFSGRGCSEPRSHRCTPSWVT EQDSCRK
11715	25616	A	11817	228	343	LLQYSIQNEDAGWAWLTPVIPTLWEAK AGRSLEVRSL
11716	25617	A	11818	322	407	VLRMLLHCLRECKLVQPLWKTVMQFLKD
11717	25618	A	11819	119	1	WEKIVRGKKCKQKENTHTHTHTHTHTHT THTYRESKRERLV
11718	25619	A	11820	269	1	FVQVFYILWTQSFCLTCCQWFLG YHLS SVSNRFRMRSGKSTFFFMTEFFFFEMES RCVTQARVLECSGISAHCKLHLPGRPH SPALV
11719	25620	A	11821	217	389	EHIETVYKGLGISEHWGKGLFNKWLTI WKKDYSWQWMLMPVIPALWEAEVGGSRV H
11720	25621	A	11822	188	1	GSHMPCRVISSVHESMNEFFAVPTSYPA NPQPRERAWRNQREKEDKKERSQRSVGR VQAGLV
11721	25622	A	11824	126	3	KLQGGVQWLTPVIPAPWEAEAGRSPEVR SSRPASTWRNLV
11722	25623	A	11825	224	3	ALTIKKEVSAMELEGSNRIQAYGVQSIT GARDYHAAASRVPAIKGTHHHARVIFVF LVETGFHHVGQAGLDSC
11723	25624	A	11826	3	364	HELPEPLRVLTARVAMAPGSR TSLLL AFALLCLPWLQEACAVQTDPLSR LFDHA MLQAHRAHQLAIDTYHEFEETYIPKDQK YSFLHDSQTYFCFSDSIPTPCNMEETHQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KSNLELLR
11724	25625	A	11827	2	376	ARELPEPITVLRTAHLKAMAPGSRTYLL LAFALLCLPWLQEAGAAQDTTLYMLFDH AMLQAHRAHQLAIDTYHEYDETYIIPKDH KYSILHDYQTSFCFSNSITTPYNKEETQ QKSNLELLRISLL
11725	25626	A	11828	288	3	IHTKNPSVHHHHQRPKVDKTTKMGKKQS RKTGNSKKWSASPPPKHESSSPATEQSW TENDFDELREEGFRRSNYSELQEEIQT GKEVENFEKN
11726	25627	A	11829	107	1	KRSGVRLQRLVLRWLTPIPTLWEAEV GSFEVRC
11727	25628	A	11830	220	354	QGNKSFKNIIAPWLGTVAHACNPSTLGG QGGRITGHEIETILANM
11728	25629	A	11831	273	352	ENLKTGQIQWLTPVIPALWEAKAGRS
11729	25630	A	11832	239	488	SQTHCSGKTENSHGTNSDRNQVPTALHK RPSSPARFLTEAVPVPVVDYLSVAFA VSAVASQWERTGKPFNPLLGETYELIR
11730	25631	A	11833	189	294	DQTRWLTPIVIPALWGAKAGSGPEVRSSL HFPLLF
11731	25632	A	11834	1	332	GTSPEPLTVLWTDLLAMAPGSRTSLLL AFALLCLPWLQEAGAVQTDPLSRLFDHA MLQDHRAHHLAIDTYHEFEETIIPKQDK YSFLHDSQTFFCFSDSIPTPSNMEET
11732	25633	A	11835	330	175	PRELAQLGSPNVRVSRVKPRGPQMFFF FFWRQESCSVAQAGVQWHEPEQQE
11733	25634	A	11836	96	1	VFVETGSRSAQDGGQWCDLSSLQPQPP RPRA
11734	25635	A	11837	267	334	SWVQWLTPVILALWEAEAGGSP
11735	25636	A	11838	180	2	SVLEKKEKNLYKNLFTYKLLKKVQGTQ CEGRAQICSVVCVCVSVCTCVHVCAYV SSC
11736	25637	A	11839	183	2	AAPLTSSAPQAPGWKPHLAPNSPFKNFT GRGQAQWLMFVIPALWEAKVGRSPEVRS LSSC
11737	25638	A	11840	54	330	DPNGQLPEPLKGLWTAHLVAMAPGSRTS LLAFGLLCLPWLQEAGAVQTVPLSRLF DHAMLQAHRAHQLAIDTYHEFEETIIPQ DQKNSFLD
11738	25639	A	11841	117	344	IQYVKQINETEMRNNESYLNHTSLTITI HTLCLMGSYLEHFQNCQKGRARRLMPVI PALWEAKAGRSPDVRSSKPA
11739	25640	A	11842	750	968	RAQGPRWILKIPFSSPFRFLPLIPLVFL YNSPPLFPFPRTNATNNSPFPPLPPLP LPFSPPPPSPSRPPPS
11740	25641	A	11843	757	1000	VVELVWYCCLFSPFFPLPSPPLFPFPFP SPFHSFPFSPFPRPLPLAPTRPPPFPS LFQAPPLLPSCSPPPPPPSLSFL
11741	25642	A	11844	278	361	TLLFFFFFFEMESHFVARAEVQWRDLGS
11742	25643	A	11845	260	2	GSCLEGLTNRKDIHTKNPSVHHHHQRP KVDKTTKMGKKQSRKTGNSKKQSTSP PKERSSSPATEQSWMENFDELREEGFT RA
11743	25644	A	11846	194	2	TKFAKEPSPPPCWQEVFKTSPLGFFFCP RSFPVNGFPRKLNLFFFETESCSVAQA GVQWCARA
11744	25645	A	11847	219	1	SLGHTLKQSESSLFSFPGGTPLELFKPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VYDPSVPPFQVSKGGCVGFFFFFQTESC SVAQAGVQWHDLGSPRA
11745	25646	A	11848	126	3	RFFFKGLFLHFFFFFFFCTESHLSVA QAGVQWCDLGLV
11746	25647	A	11849	216	339	KCFKVGKVYKLNRETFYLAQNFFDRNWA TQKMVVKTLLLELT
11747	25648	A	11850	190	334	VSYHIEMSF FEVYNEKIHDLLVCKDENG QRKQPVRLKQFIICFEFLFL
11748	25649	A	11851	198	352	SRQGTWGIHGLECFVCLFVLFETESH FVPRLECSGAISAHCTLHLPGL
11749	25650	A	11852	371	1	PPKKLGIQVFTFPAPRAFWFVLVFKKKG FPQGNLVLPGFFSKVSIQGVPPFCRKP SGWGEAFQIGFFINRGKFFFPGLGFFL KKVFLKFLAKFFFFFFFETESHLSVAQ AGVQWRSGLV
11750	25651	A	11853	176	3	KKGFPLDWNMVKNIIVKFGEDLQISKT LHTFFFLTESRSVAQAGMQWCDLGLSHS C
11751	25652	A	11854	281	375	QLTFKKYFLGWARWLTVPVLPALWEAKAG RSP
11752	25653	A	11855	146	356	KCGALIAEIEVPLFSELDRDFFLAYSMT ELCFKRCVPSLHHRALDAVDDCLHSCS CTDYPINRSLMNAY
11753	25654	A	11856	136	1	LSILCEFFNWLIEMEYRSVSQAGVQWCD LSSLKPPPPRLQCHSC
11754	25655	A	11857	277	361	IVLRGAMWLTVPVPTLWRAEEGGSPEVR
11755	25656	A	11858	295	152	VVFGFGFFETESHFVAQPGVQWCDLGLS CSLRLPGSSNSPASAFQA
11756	25657	A	11859	1	342	GTRLPEPLTVLWTAHLGAMAPGSRISLL LAFALLCLPWLQEAQVAPVSRFPDH AMLQAHRAHQLAIDTYQSEETYIPKDH KYSLLHDSQTCFRFSDSIPTPNMEDTQ HK
11757	25658	A	11860	244	332	TIEMMLDIKIQVIFLFEFKMGRKIAET T
11758	25659	A	11861	1	339	GTRVVTICQVLHAYAHFLYFFEMEARS VAQAGVRWCDLGLSQPPPPGSSSSSSSS S
11759	25660	A	11862	311	394	GMLGAVAHACNPSTLGGGLGGWITCSQEF
11760	25661	A	11863	130	1	VEPSVRTFFFFFFFETESRSVSQAGVQWH YLGLLQAPPPGSTSC
11761	25662	A	11864	3	320	IMMYALFLLSVGLVMGFVGFSSKPSPIY GGLVLIVSGVVGCVIILNFGGGYMLIV FLIYLGMMVVFGYTTAMAIEEYPEAWG SGVEVLVSVLVGLAMEVGLVLW
11762	25663	A	11866	165	309	GLILLPMLECSDRISAHCSLYLLGSYDP SDSGSHVAGTTGTCHYAWLR
11763	25664	A	11867	208	314	GSRNKLSGQAQWLTVPVLPALWEAEVGG PEIRSSR
11764	25665	A	11868	102	1	KKFFFFFFETESHLSVAQARVQCNLGLSQA PPPRFT
11765	25666	A	11869	126	3	NNALQLHSSYCKKPPFFFLKTESRSLTK AGVQWCDLGLLQ
11766	25667	A	11870	1	273	KQLPVNFLNWRLELTGLLCTNLKSKPC MIFIILVIVKYWFLFCNIFKNHIFSQA QWPTVPVLPALWEADMGGSHGYWITTIVD FMCATLT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11767	25668	A	11871	126	2	FPKALLVVFFFFFFFFFFETESRSVAQARVQWHNPGSLQCPLR
11768	25669	A	11873	269	9	QVSGKFWPDIFYKTGEKGLQCPNFPQGHPPRGLKKKSFSKKKKKKKKSIIVGQAQWLIPVIPALWEAKVGRSPEVKSSRPACTW
11769	25670	A	11874	114	1	LEAKPGVFQSGVLLVIFFFETESHVSQAGVRWCDLG
11770	25671	A	11875	146	1	GNHLSSRVGVQDQPRQHGKTLSQLKIQKVAGPGCAHLQSQEVQVGGSL
11771	25672	A	11876	2	159	SLQFFFFFFRWSFVLVAQAGVQWHDLGSPPPPPPGFKHSPASASQVAGRGR
11772	25673	A	11877	124	240	FRFSSGQAWLTPVIPALWEAETGGSLERSSRPDWR
11773	25674	A	11878	135	5	QVLFYFYFSDSFTLSPRLECSGVTLPHCNLCLPGSSDSCASAS
11774	25675	A	11879	170	2	GFFFFPEKWKYKNSFLCFFFFFFEPEFC SVAQAGVQWLHLGSLQPPPPVFKVDAAP
11775	25676	A	11880	97	267	GHGHATLRGLCVLSLFFHIPAPSVSGTSDAECCLCVIYRLICGYISRNCLYFSDHR
11776	25677	A	11881	1	292	LPEPLRVLWTAHLQAMAPRSRTTLLAFALLCLPWLQEAGADQTVPLSRLFDHAMLHAHRAHQLAIDTYQEFQTYIPEDQKYSFLHDSQTYFCFSD
11777	25678	A	11882	93	2	KYQMGWAWWLTPVILALWEAEAGRSPETSC
11778	25679	A	11883	145	2	PPLGLRLQVQAPTGFFFFFFFETESRSPRLKCKGAILAHCNVCLLV
11779	25680	A	11884	202	1	TWWRWGVTVLRLVMNCRPCDRHKSASQLIGRVRQENGLNARVGGCSEPRSRHCTPVWVTSENPSSC
11780	25681	A	11885	42	155	GERSGLSPGVQDEPGQHSGTSSLQKILKLAGHGGTCP
11781	25682	A	11886	215	1	STMARHCPLSPMLFNNAMEVLVRAISQEKIQIGIQIGKEEVQLSLFTDDMIFNLEKRKDCSKNLLQLMNLV
11782	25683	A	11887	214	1	GYFFGLNEVLGKLEKPSLKVPQNPSPKRPFFLGFFFETESRIVARLECSGAISAHFNLCLPGSSDSPVSC
11783	25684	A	11888	215	3	WGPGFPPFSFFFFFFLROGLAVIRLKCSGTITAHCSLNLFGSSDPPASVSLVATTGHEPSITQFHSHGSC
11784	25685	A	11889	118	1	RFFIMGENPTKFFFFFFETESLLPRLECSGVISAHCNLS
11785	25686	A	11890	267	83	HCLRSGVQDQPGQHGKNPSIQIKIQLATSFKKSLKIVIPPLPFKNDKTDSSKSSCLSPHS
11786	25687	A	11891	134	2	DRLAVLPRLECSGMIFLLPLPSRFKRFSCLSLPSSWDYRCAPRA
11787	25688	A	11892	116	1	SKGVGHFLFFFFFFETESRSVAKTGQVQWCDLGSLLCLV
11788	25689	A	11893	397	475	RFVCSTIKVLRDLSSDRSNPGRFLST
11789	25690	A	11894	115	331	KNVCLFVFMKNHLNPGDEGCKSPRSRHCTPSWAAQQDSISKYICIRYLYLDIYLKSLVRLRLINQLPNS
11790	25691	A	11895	134	251	INPPVSRKKKKKKKKKKKKKKKKKKKK



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKGGGL
11791	25692	A	11896	186	402	PGKNLTLENVPRENKVGKAPGQNEPPV LGGGEYQDPGGNVKGVGPPAPGFGKDG PKRLADTFDLIEGDGD
11792	25693	A	11897	100	2	KGPPFFFFFFFFFFFFFFFFGQSGQVKLK SPKCK
11793	25694	A	11898	92	3	SVARIMPYALFLLSVGLVMGFVGFSSKPS
11794	25695	A	11899	283	362	MTYMTTIVHALWASVCLLLNHAHDPLD
11795	25696	A	11900	248	1	VMSAQPGLSVILRFMGKWSNWTGMQYTE SEVERYRDRGRARETERQRDRERENP RNRKLFFYGRFKHSPQDFMPQKVHF
11796	25697	A	11901	253	2	KLQENPFKLLNFTINLCSVSLNVPTILN INIKPSFIAPKPRCPSKFQRYIYIYPS IYLSIYLSIYLSIYLPITISKVLKDEVE
11797	25698	A	11902	179	3	LAVTKNEIMGFSTIWMEMGDINFFFFFF ETKSHPMRLECSGVISAHCNLRILVSS SC
11798	25699	A	11903	1	403	GTSSQESFGGCCVSGLIAMGTAKQGERK LLCLFILAILLCSLALGSVTVHSSEPEV IIPENNPVKLICAFYDLFFFSSFSYFF HLSFFIYYPYLFVSCFTFYIVILLSFI YSHHLSVSYSYVLLIYTFIL
11799	25700	A	11904	37	242	KGPTRDQLQHPKARLPAPLRVLWTAHLA AMAAGSRTSLLLAFALLCLPWLIDGAS HIVSLFMLFIIF
11800	25701	A	11905	1	298	GTSQHRGRKDSRTGSHSSSDHPGAKLLS TEEKQAAETMRPPSAPPRRGICIPWQGLL LSSS
11801	25702	A	11906	225	30	ACYLQKDGAFAILPDVLPDMFKGHSSLY PCQHAECDHIKNIYNCVCVCVCVCVC IVICKLNV
11802	25703	A	11907	196	320	HSSSSTTPSQDTHTHTHTHTHTHTHTH HKIPQRELLPSVPD
11803	25704	A	11908	130	3	NGFVFSPFFFFFFFEMESHSVTQARVQW CDLGSLSLPPGFK
11804	25705	A	11909	381	2	ASTCGKLTFFQHWKKIILVQQVGLQKK NSTLKRAWEFLSFFQAPPLGSPKGIN ILNKGAKLKGKTNFGPIVFFFSVLP FFGLKKFQKKVFHQKSPFFFFFFFETE SRVAQAGVQWHD
11805	25706	A	11910	138	2	SVPLKEFIISQARWLTIIPALWEAEAG RSPEVRSSRPASTWRNP
11806	25707	A	11911	231	54	IRASFGIQRICLTIFFFETEPHVSQTQ AGVQWRDLGSLQPPPRRQEQNSVSKQTK TN
11807	25708	A	11912	3	461	DAWGRVEGPPLRPPATSRWAGPTLWRM EVTGDAGVPESGEIRTLKPCLLRRNYSR EQHGVAVSCLEDLRSKACDILAIKSLT PVTLVLAEDGTIVDDDDYFLCLPSNTKF VAMAINERWAYNNSNGGTGWISQESFDV FEAYSGATLLFFF
11808	25709	A	11913	318	407	LCGRLLWMLPVIIPALWEAEAGLLKLRS MR
11809	25710	A	11914	340	5	DRVAKFSEARLFRLLFFFPFLKIFCFPR GFKIFRGVCPLLPPEFWGLFQKGPGR LFFPPLGGFFFFFFFFFFFFFFFFFFFF FFPFFFFFFFFFCHKNTLLKKVHNSI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11810	25711	A	11915	274	385	IKPQRWGETRAEKLKSLKIRVPLLLQRN AAPHQQWNK
11811	25712	A	11916	259	441	DTKLPKVNILKLNPHALKKKKKKKKKKKK KKKKKKKKSSSLRG
11812	25713	A	11917	254	402	LIVSVIDFLRWRLPLLPKLECSGMISAH CRLRLPGSYHSPASGCQLLGR
11813	25714	A	11918	223	1	NTNSPRKKFFYEVSVPVFFGVFPSP LKGSPRAFLKLAWRPPLPLFFFLEMESR SAAQPEVQWCDLGSLLQPP
11814	25715	A	11919	97	3	KPFFFPFFFFFEIESRSVTQAGVQWRD LGS
11815	25716	A	11920	154	384	KEFFLMLFFFLPPPPPPFFFLGKGLF FFPPGGGGGGQFFSIGPPPRGKDDPP SPPKMGGRGTPPPPGYFFFF
11816	25717	A	11921	225	369	GTLNLLTYKIKSWGAVAHYNPSTLGGW GKWITSGQEFETSLANVVKP
11817	25718	A	11922	116	372	MEYTNKMMAMSYNLHIYQTYKNSVIEHP TGVLPHSRVIMVNNIVLCISKQLKELLR RLMWEEHLSPGGGGCSEPRSRHCTPAWA T
11818	25719	A	11923	271	409	KKKKKKKKKKKKKKKKKKKTGGGA
11819	25720	A	11924	121	228	KKKKKKKKKKKKKKKKKKKKKKKKKKR GGGFKKKPWGGQK
11820	25721	A	11925	55	423	NKPKKKNFKLKKKKKNFFFPYPLKFFFF PKSLNFFRRVVPKISPPKKKFFFKNSPS VFFFPPLKKKNFFFLTPLKFGPPKNFFK RPPPLFFFFFFFFFFLSGNCIEKL
11821	25722	A	11926	253	443	YQHQRPKVDKSMKGRNQRKKSENSKNQ NTSSPPKDHNSSPARQQNWMENEFDLT EVGFRRW
11822	25723	A	11928	175	413	KKKKKKKKKKKKKKKKKKKKKKAGGG A
11823	25724	A	11929	490	182	RKQKIKGCKKPNPLAQGGVKKKKGKGGP FNFFLKQKGQDFLKNWNLGQKKKIPIPP QVFSLRQKGAFPGRIFFFFFETESCS VAQAGVQTLKYKNKNKIK
11824	25725	A	11930	110	2	KKIPRKPPFFFFFFFYKAGSHLVAQAG VQWHDLS
11825	25726	A	11931	169	987	YLEKIMSEHSRNSDQEELLDEEINEDEI LANLSAEELKELQSEMEVAPDPSLPVG MIQKDQTDKPPTGNFNHKS LVDYMYWEK ASRRMLEEERVVPTFKSEEKTQEEHBE IEKRNKNMAQYLKEKLNNEIVANKRESK GSSNIQETDEEDEDEEDDDDDDEGEDDG EESSETNREEEGKAKEQIRNCENNCQQV TDKAFKEQRDRPEAQEQSEKKISKLDPK KLALDTSFLKVSTRPSGNQTDLDGSLRR VRKNDPDMKELNLNINIRK
11826	25727	A	11932	161	389	SVQTHPNLRSCSVLKNAMHFYLLGYVIS GCTEPAKAIKPIDRKS VHQICSGPVVLS LSTAVKKIVGNSLDAGATNI
11827	25728	A	11933	134	289	ASTQNMGMRLRLMSSPTLLSLSLSHTHI HKHTRMHTHTHTHTHTYPTTKV
11828	25729	A	11934	128	1	IKKGEFFFFFFFFFFESHSPRLQCSGTI LAHCNLHLLGSSNS
11829	25730	A	11935	131	19	MYIGWVQWLTPVIPALWEPKVGASLEAR SLRPARTSE
11830	25731	A	11936	104	3	LKGQLIRAQWLMPVIPSLWEAEMGRSPE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VGSSR
11831	25732	A	11937	146	2	GGRLGIT YHAWNPEGFFFFFEMESCSVG QAGVQWCNLSLQPPHPGFK
11832	25733	A	11938	149	1	DKCFLCVCLFIFITYLLIYFYFFETESC SIAQAGVQCCNLGSPQPLPLA
11833	25734	A	11940	176	380	QSVACLPRLECNGMILAHCSLHLLGFKR FSCLSLPSSWDYSRLRNYQGGRRWSKTH QAWCQSLTILWN
11834	25735	A	11941	133	415	KKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKSG
11835	25736	A	11942	222	420	QGDKFLDNNNSTILYMEKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKYSR
11836	25737	A	11943	163	425	KNPPKNSQLSPSTLKKKKKKKKKKKKKK KKKKKKKKKKKKKKKTG
11837	25738	A	11944	143	3	KMGKKQSRKTGNSKKQASPPPKERSSS PAMEQSWTENDFDELREE
11838	25739	A	11945	200	3	QNSQVGYKGAPHKEKTMALQARVNLGPP RGPLKRPALFFFFFETESPSVTQDGVQW HDLGSMQPP
11839	25740	A	11946	221	3	RKIEGGPSTSRKSVRGVRCFQPLGLGFP GGLFFFFFFYETESCSVARLECSGVVSA HCILHLRSTNEGRRGR
11840	25741	A	11947	68	177	ISSSFKNKCLCEKKKKKKKKKKKKKKKK KKKKKKRK
11841	25742	A	11948	210	329	RHTHTHTHTHTHILSLSLSHTHTHAHTL MYFLAFFDLRS
11842	25743	A	11949	183	20	LGTVAHSCNFVFSLSRGFLHVGNGLRL PTSDDPPTSASQSAGTTGMSPTWPE
11843	25744	A	11950	232	329	VGIKMSISSDEVNFLVRYLQESGFSS AFTF
11844	25745	A	11951	412	239	LFYEKGSRFVSQAGLELLELKQSPCFGL PKCWDYRHEPPRQADLPFCVPSSAWASW L
11845	25746	A	11952	310	393	PHTDISGTPEIMHYVHVHRTVTPQPNKP
11846	25747	A	11953	193	3	LSSWPTLISGAFKAENAVEGNDDSRIL RGFFVLFCFVLFRRQSLALSPRLECSGV ISAHCNL
11847	25748	A	11954	185	416	SVQTHPNLRSCSVLKNAMHYLLGTPEPA KAIKPIDRKSVHQICSGPVVLSLSTAVK KIVGNSLDAGATNIDLKLDY
11848	25749	A	11955	100	1	AHLSKVFPFFFFFFFEMESHVTRLECSG TISAH
11849	25750	A	11956	35	521	KEKFFFHAGVYWGPPRNFLKRAPLFFFF FFFFFFFFFFFFSFFFS
11850	25751	A	11957	214	1	KKKIFFFKEIFYPKLSRKKKNFRGAGK ILNLSIFPEKKKIFSPSFFETESCTV AQAGVQWHVLGSLQP
11851	25752	A	11958	114	1	RYFSGQAQWLTPVIPALWEAEAGRSPEV SSSRPAWLTV
11852	25753	A	11959	188	12	SKCQCTFFSNFKKTEMESHYLAQAGLEL LGFSHLPTSVSQTVGITGVSHCAQPNAL LY
11853	25754	A	11960	241	556	SSIPFLPNKHLLLSFSTLSSLGREVSIQ DMCQGTQKQFPFPLPHVFLSIRDGE LCVGRDVHLTCQTDLAQVFCVFLVGLV LSLPRAGVQWCHLSSSQPPPP
11854	25755	A	11962	362	462	KIGQALTPIIPLLWEAEAGASPEARSSR

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						SAWPT
11855	25756	A	11963	43	2	CCCYCCCCCYCC
11856	25757	A	11964	30	415	GLGFKQKIFFFFLGQGPNFLLRAKRR PFLPPPPFPKPKNRGVFLGPGSVKPK RPRQGDVPLKPRSLGVFLTSKKTPLGP WANPPPPPGDGP
11857	25758	A	11965	149	2	SKTWLKLAKYLKNTYPGWVRWLPIVPA LWQAGAGELHEPRNLRPAWAT
11858	25759	A	11966	179	3	KKNIFPPPPVKFGPPQGFFKRPPPLFFF FFFFFFFETESRSVAQGVQWLSIGSLQ AP
11859	25760	A	11967	245	382	DVTDSKMHDPDRSSHVKMWLGVAHACN PSTLGGSRGQEFKTSAN
11860	25761	A	11968	264	10	LSTLECKGVSPGVFSPKGRKGLGYIFS PFLEKPHIPLGISMYFFFFFDGVSVAQ AGVQGRDLGSLHLPSPGSSYSCASASLS S
11861	25762	A	11969	326	406	RLLKGWALWLTVPVITLWEATVGRSPE
11862	25763	A	11970	120	1	KGYGFPFPKPLGPPFFFFFATESCSV AQDGVQWRDLGS
11863	25764	A	11971	84	370	RNGAELKTPLAGQTQITINCRYSWVTLV LGDLESILCWHIFKKTNLFCGFFSSFL LGAGRMKSHCVVRLECRGMISAHRNVCL LGSNDSPCSAF
11864	25765	A	11972	196	3	SRGKMGEYFPVLFKNPSWAKAGGNKGNP FFFFFEAESCSVAQAAVQWCNLGSLQAP PPRFTPRA
11865	25766	A	11973	559	644	KIGCSAYGVAILLFLYFFNKLAFTLWKK
11866	25767	A	11974	3	391	HEAQLPEPLMVLGTGHLAEMAGGSRTYL LLAFGLLCLPWLQEAQAQTVPLSRLFD HAMLQAHRAHQLAIDTYQELEETIYPKD QKHSFLHDSQTSFCLSDSIPTPSNMEET QKSNLELLRISLLIE
11867	25768	A	11975	138	365	LKFECHSTLCANHGKQTFTFVFNKFL KYTFYFVLTYYAINWYIKNLINVFKKKK KKKKKKKKKKKNFKKKKN
11868	25769	A	11976	275	433	MSILDLSKARNFFLSFLETGSCSITQAG VQWLNHSSLQPQTPLRDPASASQ
11869	25770	A	11977	108	3	RCGLFFFETRASPCRPGWHNLGSLQPLP PRFKRF
11870	25771	A	11978	270	408	FENNVWLGRAQWLTPVIPALWEAQAGRS PGPENQNHDPYKGNPWPY
11871	25772	A	11979	228	441	QALKFVTEMLLSLKKCLDVSVIFNRHKK IELLQKKKKKKKKKKKKKKPSQKKKD SSRGKDS
11872	25773	A	11980	2	447	GALALNKTADVWRLNFLVSGLHWKRWL QOTSLSKWKIKECSILKKKKKKKKKK KKKKKKKKDKK
11873	25774	A	11981	124	445	KYGEMSONPARGGPKFSKNQKYSEHLRI HCCPPFTFLISKKEIGDRKYSICKSGCF YQKKEEDWFCPCQKTKTSRRAKSLKRP KQKPVAPPGGVKAPAKPRSLPRF
11874	25775	A	11982	48	429	KESNGSQDRLLPKIHSFVSGGKSGGMS QNPARGGPKLSKNQKSEHLRIHCCPPL PFLISKKEIGDRKYSFGKSGCFQKKKE DWICCPQKTKLKGKIRPPPKKNGPGGS LNGRTTWVSGLFVHN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
11875	25776	A	11983	419	500	SLLVKVEKQWP GAVAHACNPSTLGGPG
11876	25777	A	11984	362	496	LWSPIRILLRRAWWHVPTVPATWEAEVGRILLEPRSLCNMVRPIS
11877	25778	A	11985	142	433	RFVCSTIKVLRLDSSDRSNPGRFLSTNSLKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKGGGGVIKKFLGGPIFGGGGKEKFFFFGGGFIN
11878	25779	A	11986	177	2	CQRRWVTLSHHTHSITRPLGQLKKGWSPGAVAHTYNPSFLGGQGQGWVTYVHRTGRTR
11879	25780	A	11987	178	443	DKKKKKKKKKKKKKKKKKKKKKKAGGLFKKI
11880	25781	A	11988	329	410	LIIFFIFFERESH SVAQAIVQWHDLG S
11881	25782	A	11989	146	1	DRASALQPGRQRNFVSKNNNNVIYITNTLTITIFLGTTYDALSP EL
11882	25783	A	11990	240	420	GVFAPLLGDVSQS GYTGF RDPLEEAVCLFLELECHAERTTALFRAVRQGC SLQNLSVAF
11883	25784	A	11991	239	410	GTLFIYLLGDLFIYFRNKSLTLLPRLEC GGIVIAHCSDL LGSGYPSISALPSSWD C
11884	25785	A	11992	126	3	YTGEYKSFC HKDTCTHMFTAALFTIAKTWNKN GRVGGRV
11885	25786	A	11993	300	22	SQLLGR LRQENHFNWGGRGCSEPRSCHCIPAWATRANSIFCGFQASSVEVRRSARKKLFSIDILKRHNTISRVRSGLLLVDSYFGRLATPVRAQ
11886	25787	A	11994	303	2	EGETIFLPSPPPFP PGQENPGSNCSPPLFPFGTFLDIRVAGSHKVQAKGVFKKRPPSLHLFLIKRFFFFFFETESRSVPQAGVQWRDLGSLQT PPPGFKR
11887	25788	A	11995	171	457	SFSDHLILGWIGFCNNLSKIALCSSPIKNKND DLQKKKKKKKKKKKKKKKAKASSSYQDSS
11888	25789	A	11996	357	204	EKTGFPHVGQAGVDLLTSRSTRLSLPKCWDYRHEPMRLAGHLYFYFPQM K
11889	25790	A	11997	219	1	PRVFWAPP PRYP PGALFWAPRVGVSLGARAPT KAGPKQKGARGTFFFFFEMESHLSRPLECNGTIWAHCNL C
11890	25791	A	11998	254	1	AHLRGNRQLPKHTTFQYMTTNLKCAFSVGRQSYSIPWRSFYTSLFFKYSCVFHTHTHTHTHTHTLYFQIMVLLPSLRKKGS
11891	25792	A	11999	167	2	NFKSFFQGLSRGVLPKVNLF FFLETESCSVSQAGMQWGDLDSLQPPP TRPPTRP
11892	25793	A	12000	104	3	RPWTFFFFSETKRSVAQAGVQWRDLCSLQPPP
11893	25794	A	12001	178	2	KIFORGAKNSPWGLPFRGGENKKGAPPCQKGFGRFFFFFFFFTESRFITQTGVQWC DLGP
11894	25795	A	12002	163	282	GIGGEWCLS KYVIKYVKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
11895	25796	A	12003	195	2	KWGR IPLKGGGFCFTKKKSGQTLLIKSPPPAFFVFFIFFLETESRSVAQATVQWCDLGS LQAP
11896	25797	A	12004	152	1	CFVDVSAELRLPKDFMTKTPKAMATKAKIDKWALT KLKS FCTAKETI IRV
11897	25798	A	12005	359	1	EVVPIWPPPKRRVLSKVSQKFISAPIR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKPFPCQVGLILAPFRVLLIGRPFFFFF GVLVVEIQRWSFISLVVVVRARIMMYA LFLLSVGLVMGFVEFSSKHCPVYGALVL VSIIGRV
11898	25799	A	12006	189	12	DGRLPGSVCCYILIFLRQSFTLLAQAGAQ WCHLGSLSQPPPGFKRRVSRIRAVRG DQ
11899	25800	A	12007	131	3	KIFFFFFFFFEMESHSAQAGVQWRDLGS MQDPPPGFMPLLFY
11900	25801	A	12008	150	2	IILFLVPIEAVFFFFFFETVAEAGVQWHNL SSLQPPPPGFKQSPASARVA
11901	25802	A	12009	305	3	KFFSLKASIRGRWFGLEFPPKKGFLP KIPHOVFKGGLWEKLQLGKAGLNLGPY KGFFKGAARFFFFFFETESRSVAQAGVQ WRDLAHSVHASAHAS
11902	25803	A	12010	263	517	DKGFQLPPRWCPGDPLFFYGGIVFHGG YGPFFFFFFFKAESRLVAQAGVQWQDLG SLQPPPCRTTRGSP
11903	25804	A	12011	107	374	WMGTWGSPLVLLTTRSTCPPRSPRLHRR TGATIWIFFRLFETGTVLPMLECSIVIM AHCRLQLPGSSSSPTIASQVAGTKAHL DCFVY
11904	25805	A	12012	144	261	FPKINNFFYFTFLQDPTGIFSLDKTIGL GTYGRIYLV
11905	25806	A	12013	371	3	IFHLRKIFTFLPGIFWPRIILSEKKPK RFWVKIKKFKNGYPLKNIPKYGPRF FFKGEKNPNKVPVLKKIKIPSFSGALG FLQKKASKPFFFFFFDTECTVDQSGVQ WCDLGSQAP
11906	25807	A	12014	101	3	RGAFFFFFFFFETRSRSVIQAGVQWCDLGS LQAP
11907	25808	A	12015	205	2	VFNPSGINVMYVDAILNKRILATRIQQH IKQRIILHDQVGFHGMQGWFSIRKSNV IQHINRPKDKN
11908	25809	A	12016	168	1	GCVCQFQKKLGNGLNGFFFLFFFFFF EMKRSRVQAGVHWRYLSSLQTPPEFK
11909	25810	A	12017	311	2	RGLRFGQWKTQMNPNTPFSALRPGQLS SIRSGLLHTYPGLGDRSEPLSCSILSSS KYVVWQAVTSALSSNKPASQGHWKDDF FLFFETESCSVTQAGVQWH
11910	25811	A	12018	383	247	LVEMGFRHVQDGLDLTSSQSAHLGLPK WWDYRREPRLATIEVL
11911	25812	A	12019	2	379	RVLWTAHLAAMAAGSRTSLLLAFAALLCL PWLQEAGAVQTVPLSRLEKEAMLQAHRA HQLAIDTYQEFISSWGMEAYITKEQKYS FLHDSQTSFCFSDSIPTSSNMEETQQKS NLELLHISLLIES
11912	25813	A	12020	3	389	PEPLRVLWTAHRGAKGAGSRTSLLLGFA LLCLPWLQEAGAVQTVPLSKLFDHAMLQ AHRAHQLAIDTYQEFETYIPEDQKYSF LHDSQTSFCFSDSIPTSPNMEETQQKTN LELLRIFLVLIELWLDL
11913	25814	A	12021	247	386	PMLGHVSQSGNGVRDPLEEAVCPALAKL KHCSGRSTALFRAGRQKR
11914	25815	A	12022	17	371	PLRDLWTAHLEAMAPSFRTDLLLAYALL CLPWLQEARAVQTVSLYRLSDHAMLQAH RAHQLAIDTYHEIETYILKDQKYSFLH DSQTSFCFSDSIPTSPNKEETQQKPYLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLPISL
11915	25816	A	12023	3	359	LRALWTADLGAKAPGSRFTLLLASALLC LPWLEEAGAGQTVPLSKLFDHAILQHR AHQLAIDTYQELETYIPKQKHSFLLD SQTSCFLDSIPTPSNMEETROKSNLEL FRTSLLL
11916	25817	A	12024	2	363	PEPLKGLWTDHLGALAPSSRTSLLLAYA LLCLPWLQFAGAGQTVPVYTLFDHAMLQ AHRAHQLAIDTYHELDETYMPEDHKYSF LHDSQTCFCFSDSITTPYNMEETQHTSN VELLRISL
11917	25818	A	12025	314	393	GQAWWLTPVIPAFWEAKGGRSLEARS
11918	25819	A	12026	80	392	PLIACSFFLFLFFFGKKILFLPPRWKG GGGIWVNGNPGFRGQAFFLASSSKKPGM GGPPLTPGKRFFVLKKKGFSPGGPGGSK FSAPGTPPTGPPKGWEIPAK
11919	25820	A	12027	165	2	WQKLLFHFGTESCSVARVGVQRHFSPP KPPPPPEFKQLSAPASRVADRRPPDAW
11920	25821	A	12028	1	338	VFVALKFLMCLLSVCFSLNENIYNSLP QKNCLPLIFFFLFFEMEACSVTQAGVQW GDLGSLQPPVSHLNLGGGCCEPRECHC TPCSRPGDRDFVFNKNTMIQDNHLMELT
11921	25822	A	12029	2	315	HEERERERERERERERERERVGRVTG VGGETYKAELPRVGGAAQKRAHFSARGR LFMEICGDMCGEKGKPPHSLTECLSR CGERFFDTSLAITRGCAQSV
11922	25823	A	12030	216	3	ERIIPRGVRQNRFLFSGRDTASPLFYF PPRQIHKRGVEDREHRRGERERERERE RERERERERARAAR
11923	25824	A	12031	114	329	QTERNSTININKDIIHTKTPSVGHQHRP KVDKTTKMGRNQSRKAENSKNWKASSPP KEHNSSPAREQNWMES
11924	25825	A	12032	177	1	IKKKTFFWQNIPLFSKKKTCRQKFFFFF FFETGSLPLRLVCSGAVLAHCSLCLPGS AFL
11925	25826	A	12033	127	1	PSFFFFFFFNETESRSVAQAGVQWRDL SLQAPPPGFITPSC
11926	25827	A	12034	47	314	GAPVASVSISCPSCSATDGVVRNGKSTA GHQRYLCSHCRTWQLQFTYTASQPGTH QKIIDMAMNGVGCRATARIMGVGLNTIL RHLKN
11927	25828	A	12035	15	408	GAI PGAMGHFTEEDKATITSLWGMVNAE DAGGETLERLLVDYPWTQRFFDSFGNLS SASAIMGNPKVMAHGKVLTSLGDA TKH LDDLKGTFAQLSELHCDKLHVDPENFKL LGNVLVTGMAIHLGKEFTP
11928	25829	A	12036	122	2	KLVDVLPPPGGARVFFFFFFFPLETEHCS VAKAGVQWHDG
11929	25830	A	12037	154	1	GKPPPKLGFWGGPRQVRGRGPPFFFFFF ETESPSVAKAGVQWCDLGS LHLPL
11930	25831	A	12038	58	254	DPRVRQQRRTAHCSLNLPLGLQRPPSL PSGWDYRHAPLCATQKILAYRVAQRERS AHGSYYQAS
11931	25832	A	12039	270	124	DGVLLLLPRLECNCAISAHGNLRLPGSS NSPASNKTQNNNKKTL SNKF
11932	25833	A	12040	63	355	LGRGTAHRLWRPLSRPASRVSYLSAAT NKRSFAPP SRAFPWDNWERGGFFYFET GSHRRRPGRMECSGAITAHCSLDFPGSE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11933	25834	A	12041	184	3	MGFTMFPSLVSNS GVSRLLGGVSQLGYMGVRDPLEEAVCLF SKLKHHHPGRRTALFRAVRQGCLSLQKFL LLFA
11934	25835	A	12042	118	3	DRVLLCYLGWECSGTISAYCNLHLPQSK RFSCLSLPSS
11935	25836	A	12043	40	436	LSEGKLTNRKDNHTKTPSVHHHHQKPKV DKTTRMGRIQSTKAENSKNESTSSPPKE HSTSPATEQSRMENDFDELRDFRRSVI TNFSELKEDVRTLCKEAKNLEKRLDEWR TRINSMEKTINDLMELKMA
11936	25837	A	12044	101	2	HLGQVRWLTPVIPILWEAEVGGSPPEHRS SRPAW
11937	25838	A	12045	123	3	LTVIKELPLGQARWLTPVIPALWEVKVG GSEPEVRSSRPA
11938	25839	A	12046	3	432	PIFGGGERIFPFFFFFFSQGGGVFFPKT KNKGFFPFLGFFKKIFLRNFFFLFFPFF FLNPFYFGAPPPFFPGGFFFFPLFS RFFKFFQNFPPQGGFFGGFFFLGFF FFFFFL
11939	25840	A	12047	325	164	KNKRKNRGQARWLTPVIPALWEAEAGGS PEVRTTGVSHGTRPHLLNTVSEYI
11940	25841	A	12048	187	381	LMDKRVSLWGDENILKVESNSGCTTLYL LVCFEMESRSITQAGVQWRDLSSLQPPP SRFKRFSC
11941	25842	A	12049	84	464	SYRVPSHPDTLVLSRISAQEAAGEKSPFC FPERVWPCPRPLSDLGRRLKLECGPDL DSTFLSFFEGGLKTGSHSGALECSGVI RDHCGCLCSGSGDPPISACLVRAGTTGV SHHCIFCRQDLPGS
11942	25843	A	12050	232	20	LLQCSSRAKIHTSLTGNQKLEMIKLSSE GMSKAEISQKLGLLHHLGLVANAKQRF KVIRSATPEFRHAE
11943	25844	A	12051	401	518	FFETESCSVTQAGVQWRNLSPLRA
11944	25845	A	12052	191	1	LFPLKKEKILFLGPGTNGAPPMFFLKAP PLFFFFFFFVFVFVFVFVFVFVNLFL LSFLHILEP
11945	25846	A	12053	12	369	PLPIYSACIEVGSNPQPGIDAKSVSHN NCYLKEKKKKSNGSQNNLLPKIHTPENG SGKKTGEKIQNPPRGGPKLSKNQKYSKN LKKHCCPRLTFLISKREKGNRKYTFGKS GCFYQKK
11946	25847	A	12054	89	513	NFTVRGSIPLNNIPMANLLLLLIVPILI AMAFMLTERKILGYIQLRKGPNVVGPI GLLQPFDAIPLFPKEPLTPAPSAFALC FAAPALALPFALFLCPRPLGRP
11947	25848	A	12055	158	3	SQLTWPIMAQTDSMCLWIVYFDDNIGWA WWLMSVPTLWEAKVGGSLHNS
11948	25849	A	12056	113	1	KSHGGHGVFVLVSVLVGLAMEVGLVLVW KEYDGAALA
11949	25850	A	12057	44	263	ARIARSAHEGKMPRKYTGARKNAENRPO RELQLKASRSTIDLAHACNALWYQLFL ISVGSWKNYILFYLYT
11950	25851	A	12058	142	1	KKIFFRYKKEGFSFPKFFRISLFFFFFF ETESRSVAQAGVQWRDLGS
11951	25852	A	12059	12	347	QTERNSININKDIIHTETPSEGHQHQRP IVDKSTKMRKNQCKKAENSKNQSSSPA KDHNCPLPAKEQNWTENEFHKLTEVGFRI



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ITNSVELKEHILTQCKEAKNLEQRLEEL
11952	25853	A	12060	245	3	MPEGSFFLEIPEITRVFVKPGKFLGGV GPSLLFFFFFFFFFFMRQSLAVSPRLEC NSAISAHCNLCLLGSSDSRSSGSR
11953	25854	A	12061	94	3	KGGIFFFFFFFFLQSPSVAQAGVQWCD LG
11954	25855	A	12062	108	5	NNLSSGVRDQPGQHGETTSLKIQKLAR HGGRHL
11955	25856	A	12063	298	1	KKKKINTHAQKRGPPFFFKPPPEKGKAP PPQRVTKKGGEKDSFIPKRREKKNPPPL SFFFLVVRVHRERERARERERERERER ERERERERERERERER
11956	25857	A	12064	122	1	VCEGVCVGGWVRDRERERERERERERER ERERERERERAR
11957	25858	A	12065	126	1	ATCTKFRNDNRALLRVRFERERERERE RERERERERERERESR
11958	25859	A	12066	48	351	FFFFFFFFKKGPKIVPPGGGGGGDPIFL EPPPPPLKKFWGPPLRGRNGKGGPPGW VNFGIFLKKKGLPWGPGGVKTPAFKGS GPTPPKGGNNRKNPPPW
11959	25860	A	12067	1	365	GTRLTVLWTAHLVAMAPGSRSTSLLDFA LLCLPWLQEAGAVQTVPLSRLFDHAMLQ AHRAHQLGIDTYQEDEETYIPKDHEDSF LHDCQTSFCFSDSIPTPSNMEETRQKYH LELLRISLLF
11960	25861	A	12068	174	1	PAWVMQHNVPVSLFFCFETESRSLTRLE CSGTISAHCNVRLLPGSSDSPVSPSRVAA RA
11961	25862	A	12069	270	375	TRIKRCNGGRAQWLTPVIPALWEAKAGE SPEVRSS
11962	25863	A	12070	197	350	KKIYIFLTINTIMDLIIPFLDNILGFW LGAVAHACNPSTLGGRGCVITRS
11963	25864	A	12071	3	378	HEGQLPEPLKGLWTAHLGLMAPGSRSTSL LLAIDLCLPWLKEAVAVQTVPLSRLYD HAMLQAHRAHQLAIDTYQBIETTYIPKD QKLSFLHEYQTSFCFSDSIPTPSNMEET LHKSHLELLRIYL
11964	25865	A	12072	219	1	FSHPFPPGVFQTPLVFPRPWEVLGSPGG GGGPPKKWAGVQKWVFFFFFFFWEMESC SVAQAGVQWYDLGSPRA
11965	25866	A	12073	134	3	VFGPPFFFFFFCETESHSAQAGVQWRD LCSLQAPPPGFMPS
11966	25867	A	12074	175	357	MPINQPVKKMCVCVCVYIYIHTPLYI RVYMYMCMYICVYIHVYIWMCIYIHTHV STYVW
11967	25868	A	12075	193	350	KIPHLTSLYHTQNYLKYCIGQAWLTPV IPALWEAEAGGSPEVRSSRPAPWP
11968	25869	A	12076	252	1	GVFGFPFKKGGFFWVGFLGTPQIFWVG VFFKKKGALWVKGLLGKPPPPPLFFFF FETESCSVARAGVQWRDSVKKKITARA
11969	25870	A	12077	273	366	IFIYLFYLFETESCSVSQAGVQWPNLG RLR
11970	25871	A	12078	127	2	KKKKTLFFFFFFFEMESRSVTQAGVQW CDLSSLQPPPLV
11971	25872	A	12079	206	334	HNRVTIVNNLIVHFKITKRCWTQWLTP VIPALWEAKAGGSSE
11972	25873	A	12080	135	2	KMKRKFGEQSQIPKTLQTFFFLTESRSV AQAGMQWCDLGLSHSC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11973	25874	A	12081	147	3	ATTPGLFFIFYPFETESHIAQAGVQCMISVHCNLCPLPGSSDSPVLV
11974	25875	A	12082	106	2	YFIPINEGYCFIYLFFETESRSVVQAGVQWCDLV
11975	25876	A	12083	164	346	CPYKKRKKANQAKWLTFVIMLFGRPRRVDRPSSGVQDKPGQHGETPSLPKIQKKSQAWWCA
11976	25877	A	12084	186	1	KSLSFGKNPLFKGPPPPPPPPPPPPFETR SRSVTQAGWGAVIMAHCCNLNLPGPSDDP TPAPRA
11977	25878	A	12085	98	2	CPFFRVNFFFFEMESRSVAQAGVQWRDLGSRA
11978	25879	A	12086	154	2	SPTPEKGVWELPSPFFSWGPKIWGCIFFLYETESGSVAQAGVQWRDLGS
11979	25880	A	12087	326	3	KTSVITCGLPMGWSWGPFPKGPWWCKKF CVCKFWANQTLKKNLQAGRFQKPFSAALFLEMGGFPFKFRFFQGSQFFFFFETESCSVTQAGGQWNLGSLRPLPP
11980	25881	A	12088	154	3	KEFSFFAPGGKQGEIRSLRGPPPVQKPLFFFFFETESRSVAQAGVQWR
11981	25882	A	12089	174	2	SWKAILQYSLEIILYLPFQIFLCFSHTHTHTHTHTHTLYSQIMVLLLP SLRKGSG
11982	25883	A	12090	265	30	WFIYSEISQLWGLPSFNTLGTWQSLSFIFVAMRSCCVTQAGLELLASSDPPVSA SQSARIRAMSPSVAVVIPGRSR
11983	25884	A	12091	257	1	GSVMRMHTEEQYPENKVEQSSSGFIRPHLVYRVCFYLSVCLSVCLSIYLSIYLSIYLSFFLSFFLLRKSILYLSIFLSFFLLSPRV
11984	25885	A	12092	311	404	LYHQNPWLYSVFFLETESCSVAQAGVQWCD
11985	25886	A	12093	331	83	GDDYKGARENSRDDKLFVILIMMVVIQLHVFVKIHKTLQLNGYILLCKLYLINLTKNNFQKPKTNSQKTLHIHPDSTAANI
11986	25887	A	12094	82	2	LREPNNLPGGEGCNARWCHCTPAL
11987	25888	A	12095	255	393	HGILFSSFVCNLSQFLSQHWLMPVIPALWEAEVGGSLPRSSSTLAW
11988	25889	A	12096	80	3	PPPPPPPPFETESRSVARLECSGMI
11989	25890	A	12097	367	1	PRVDKPTKMGKKQGRKTGNSKKQSPSAPPKERSSSPATEQSWMENDFAKLREEGFRSNYSELOEEIQTGKEVETFEKNLDECITRIPNTEKCLKELMELPKPAQELREEC RSLRSRCDQL
11990	25891	A	12098	94	236	MWADYFCMSPSIDGLKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKGGAP
11991	25892	A	12099	410	212	NSLHPSTSLFRSSHFIKLISGQAQWLTPPIPVWEAKAGGLETRSSRLAWAAQEDPIIMPVCK
11992	25893	A	12100	140	324	NLGQAQWLMPVIPARPWAEVGRSLAVRSSNSPASASQSAGPTGPHHNWLMFLQLLTRL
11993	25894	A	12101	247	357	KQIQGRAWWLTPVFSPLWEAKAGESPEVRSLRPAPWT
11994	25895	A	12102	245	2	DVLVGGCLPAGGTLHLTSIFLLSGCWC GSKDEEAPCKQRISVQRESQSRTRLRAGVSPKKAHPCEMCGLILEDVLHFPDLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11995	25896	A	12103	230	379	KEASFFETESHVSQAGVQWRSLNPLGS GNPPTSTSRVAGTTGMSHHVWL
11996	25897	A	12104	86	2	DGVSVLSPRLECNGLILAHNCNLRPLGSS
11997	25898	A	12105	116	2	SQKTPFFFFFETVSLLLPKLECNCAISAH CNLCPLGSSD
11998	25899	A	12106	271	416	QFTFSKAFNLVFIKPSFHISFYRTHYSQ AWWLTPVIPELWEAEAGGSP
11999	25900	A	12107	194	3	HVLGTVLVAEDTASNKIRSLQGCLLLPL LFSVLEVLARAIQKEIKVIQIGREE VNRRRGR
12000	25901	A	12108	142	3	LCLLYWDCKRHAWWRGQVRWLTPVIPAL WEAEAGGSPEVRSRLPAW
12001	25902	A	12109	233	346	HQRSLIGWAQWLMPIPALWEAEAGVSP EVRSCLKPAWP
12002	25903	A	12110	234	349	GFSPFYDFCLFVFETESCCVVQAGVRWH DLGSLQPPPP
12003	25904	A	12111	136	333	RLNFFFYFYFFETASCSVAQAGVQWHDLA HCIPAWETEQDSISKNTVQKRKKKVTRA GISKTKNENF
12004	25905	A	12112	345	110	QDGLCLVMTLQETQPILAYSLWFFIVFP TTKACNVQGD SKFLKKKYLGGVQWMLP VIPTLWGADVEGSPELRSLEPA
12005	25906	A	12113	108	285	YNAMKNRFLKTI LNKNKSIGWARWMAV IPALWEAKAGRSPEVKSSRSRPGAVAQV DAA
12006	25907	A	12114	1	364	RVVAAEMGKFMKPGKAALDLAGRYSGRK AVIVKNIDDGTS DRPYSHALVAGIDRYP RKETAAMGKKKI AKRSKIKSFVKVHNYH QLMPTRYSDIPLDKTVVNKDVFRDPAL KRKARREAK
12007	25908	A	12115	120	3	TQIWGAFLTLFFFFFFFEAKSHSVAQAGV QWCSLGLSLQA
12008	25909	A	12116	120	3	TQIWGPFLTFFFFFFFEAKSHSVAQAGV QWCSLGLSLQA
12009	25910	A	12117	231	1	FLSPFSCYSATTKLLSLSYFLLGHILL LGSTPEAAAQVVQWVSFADSDIVPPAST WVFPTLGI MHHNKQATENAKE
12010	25911	A	12118	216	1	LIFPPLLNFCYGEVLGFQGFALFFACM FFWPRFSPKTTTTFFYEKEFHSAQAQGV QWCDLGLSLQPLPRGFK
12011	25912	A	12120	267	1	KKKKKAFPSPLLGCFFIRLQKHLGLILV YRSHLISSLLCLEGIILSLFIIATLITL NTHSLLANIVPIAILVFAACEAAVGLAL LVSIS
12012	25913	A	12121	167	372	ISGQDLLKETKRVKRPFQQDDVPFINIF VPTPGAPRSLRQILELRGKTDPSP IIVG DFNTLFSALDRS
12013	25914	A	12122	124	2	GLLKFNIFAPFFFFFFSETESHVSVAQGV QWCDLGLSLQPPPP
12014	25915	A	12123	121	1	RFTAASANSAGAVSAAGVGMGDPGSEIIE SVPPAGPVSSV
12015	25916	A	12124	176	2	RDLRGFSRFSNYKFWNFRVGGIFKVFV GKGVKRFFFFFFFETESCSVAQAGQWRD LG
12016	25917	A	12125	137	2	KLGFFGGGGGKIFAPQKNFFFFFFFEE MESCSVAQAGVQWRDIG
12017	25918	A	12126	103	3	LEENLGNTIQDIGRCKDFTSKTPKAMAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KAKID
12018	25919	A	12127	212	351	LITFEILNICLGDNILDGLARWLTPVI PALWEAKAGGSPEVRSRLR
12019	25920	A	12129	187	3	RGSTMQQTNTRTPGVRVLYIILMIATMA IPYIPMANLLLLIVPILIAMAFIMLTER KILGY
12020	25921	A	12130	13	329	ASRVITIRVMASNSTKSFLADAGYGEQEL DANSALMELDKGLRSGKLGEQCEAVVRF PRLFKQYPPFILINSAFLKLADVFRVGN NFLRLCVLKVTQQSEKHLEKI
12021	25922	A	12131	231	330	MDTDEIYLGRAPWLTPVIPALWEAKASG SPEVR
12022	25923	A	12132	95	2	KGKCFPPFFFFFETESRSVAQAGVWRDL SSL
12023	25924	A	12133	129	1	DLALLPRLWCSAMIMAHCNSELSSSDP PISASQIPGTIGMCH
12024	25925	A	12134	196	361	TIMEYYAAMKKKSESPLLFHQGKKLNQD GGAWWWPTPVIPALWKARTGGSLEPRS
12025	25926	A	12135	120	1	PPPPGLFFFFFFFETESYSVAQAGVQWCN LGS LHPPPPPEFK
12026	25927	A	12136	235	3	KKGIRIERDRLKQLSVCQRFQAKFPFPF PSGVGEKQNFFFKKKKKKKGRAQWLTPV IPALWEAEAGGSFEVRSRPA
12027	25928	A	12137	185	1	IWCPFFFCPGPOICSFRCFFFPFFFPFF LEAETRSFAQAGVQWCDLGS LQSSWVTE LAAAS
12028	25929	A	12138	158	1	LRRGGVFSIFFCGGTMVLSPADKTNVKA AWGKVGAHAGEYGAELERMFLSF
12029	25930	A	12139	76	3	KVLARAIRQEKIKDIQIGKEEVK
12030	25931	A	12140	157	2	FFSSPRLLKRRPGNFLGARENFFFFFFFS ETESPSIAQAGEQWRDLGSLQAP
12031	25932	A	12141	234	388	LSQLMSANLFFVLLFEAEFHSVNRLECS GMIWAHCNHLPGSSSESPASTSQ
12032	25933	A	12142	112	453	LGRRQAASMREGISIHVGQAGVHIGNAC WELYCLEHGIQPDGHMPDSTIGGGDDSD FNTFFNETGAGKHVPRAAFVDLEPTAID EVCTGTYRQLFHPEQLITGKEDAANNYA RG
12033	25934	A	12143	44	443	AKLGTRKLPKAKMGKEITLINIVVIGH VDWGKTTTTGHLYKCGIDKRTIEKLE KEAAEMGKGSFKYAWVLDKLKADREGER TIDISLWKLDTSKNYVTIIDAPGHRDFI KNMITGTSHADCAVLIDAAGV
12034	25935	A	12144	3	386	REAATMRECICIHVGAGVQNGNACWEL YCLEHGIQPDGHMPDSTIGGGDDSD FFSETGAGKHVPRAAFVDLEPTGIDEVR TGTYRQLLHPVQLITGKEDAANNYARGH YTIGKEIIDLVLDRI
12035	25936	A	12145	3	386	AGATYIDRLRVALFEATFTLWVRPELS SGEATMRECMSIHVGQAGVQNGNACWE LYCLEHGVQPDGHMPDSTIGGGDDALN TFFSETGAGKHVPRTTEVDLEPTTEIGEE GTGTYRQLFHPEQHMM
12036	25937	A	12146	3	385	GRATYIDRLRVALLEATTSTLRLRREL SREATTMREGICIHVGQAGVQNGNACWE LYCLEHGIQPDGQMPDSTIGGGDDFFN TFFIETGAGKHVPRAAFVDLEPTDIGEI RTGTYRQLLHPQLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12037	25938	A	12147	11	381	HTPEGRTRVPVLIAGVVVCQEALRDWGR VTASSTGAMAFRLSMWGVLTALGRSGAK LCTGCGSRLRSPFSFVYLPRWVSSVLAR CPKKPVSSYLRFSEQLPIFKAQNPDAK TTELIRRIAQR
12038	25939	A	12148	321	509	YSMDQYFIPFYCQIMHLCFFLTKTRVSL FPWLECSGATSAHCNFCLLSSSNPASA SRVTGIT
12039	25940	A	12149	51	400	AATMRECISIHVGQAGVHIGNACWEL LEHGIQPDGQMPDCKTIGGGDDSFNTFF NETGAGKHVPRAVFVDLEPTVIDEVRTG TYRQLFHPDQLITKEDAANNYARGHYT IGKE
12040	25941	A	12150	25	399	EATTSTLGLRHQLGSRESTAMRECISIH VGQAGVHIGNACWELYLEHGLHPDQGM PGDQTIGGGDDSFDTFFSETGAGKHVPR AVLVDLEPTVIDEVRTGTYYRRLFHPEQL ITGPEDAANNYAR
12041	25942	A	12151	1	402	TKEEELCLACRQRADGWRSQMNAGSD PVGIVSAARTIIGSFNGALTAVPVQDLG STVIKKVLKRATVAPEDVSEVIFGHVLA AGCGQNPVRQASGGAGIFYSVPAWSCHM ICGSLKAVCLAVQSIGIGDST
12042	25943	A	12152	3	400	TDRLRVALKKTTSFPCFPHHLSRETA TMRECISIHVGQAGDHIGYACWELYLE HSLQPEGQMPGDKTIGGGDDYFNTFFSE TGAVKHVPRAVFVDLEPTVIDEVSIGTY RQLFRPERLITSKEDAVNIY
12043	25944	A	12153	2	398	GRCALDRNTFIFARFGCYLIASGHPEK LMDMDMSPLRPQNYLFGCKLKAENDYHF IVANDENEHQISLTTASLRAGANDDMNI VEAEAMNYEGTPIKETLATLKMVSQATD SLGGSEITPPSVLRLKCGSR
12044	25945	A	12154	203	405	FTCPSRRIICVISRRISPCCAPDLNPLS ANAMLDVFVTFVEDPGGWDSKNLQKKWSH YSELTGIRPKI
12045	25946	A	12155	229	397	TKIAHHKAGFALISKKITKNLKMFLSKF LPIHALWVTGSSGMQPYPLVWGHYDLGK
12046	25947	A	12156	2	399	GGVPHCVWATAWGMRLPGLPGPTGLCAQT SSRGQKSVLKQKESCGIWQLYHFLSRKQ EPRWEPCVSGSSSGDGAVADLADELRGY PALCCTLPVHSYRSWAGIRPQIMNGPLH PRPLVALLDGRDCTVEMPIL
12047	25948	A	12157	85	414	ALLPQSEALQCAVTMPHSYPALSAEQKK EVSDIALRIEAPGKSLAADESVGSMK RLSQIGVENTEENRLLYRQVLFSAADDRE KKGIGGVIFFHETLYQKDDHGVFPVR
12048	25949	A	12158	85	407	GLLPHSEPLQRAVTMPHSDPALYAEHKK DVSDIALRIGSPGKILAAYESMGSMAN PLNQMGVENTKQNRRLYRQDLFRAEDRE KKSLAGVIFFHDTLYHKDDNGVP
12049	25950	A	12159	85	406	VLLPHSEALEGAVTMPHSYPALSGEHNK ELSDIALRIVAPGKILAADESVGSMK RLSQIGVENTEENRPLYRQDLFSADDRG KKSIGGDLFFHDTLYQKDDNGGP
12050	25951	A	12160	275	146	EKTFIISFFFFFETESHVAQTGVQWHD LGSLQAPPPWFRIA
12051	25952	A	12161	212	2	KRSRPFFFFKEMGSCYIAQVGMQWLFV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GTITACYDPBLLGSKDPPTSASQVTGNT GTHHTQLIFVFLV
12052	25953	A	12162	253	2	GRVDSECCLANGNAEKSFICCLLVLYFY LSSRQSHSVQAQGVQWHDLGSLQPPPPG FSLLSRVAGTTGARHHDWLI FVFLGET
12053	25954	A	12163	228	1	LLGLWFEQLGRFTKIAKTGERSQTQSG HSMDMRVPAQLLGLLLLWFPGRCDIQM TQSPPAVSASVGDRVIITCR
12054	25955	A	12164	122	1	RLLFFETESRSVARLECSGATSAHCSLR LPGSGSSPASAS
12055	25956	A	12165	239	350	GQARWLTPVIPALWEAKASKSLEVRSLR LAWAGHGGG
12056	25957	A	12166	235	359	TDKAISKRDLSVLREIIFEMESRSVAR MECSGVISARCNL
12057	25958	A	12167	209	396	QFSGIPFDQYKCGFKNVIYIYIYIYIYI YIYIYRKYTRAYTKRYMCVFSRATHNIV YLCAYI
12058	25959	A	12168	327	130	GGVGFLLGGPGEKPPRPSFFFFFEKES RSVPQARVQWPDFGSLPAPFPFGTFFLR ESFLFSSLM
12059	25960	A	12169	317	422	RGEKPLFFFLQKKKKKKKKKKKNIKKG GRRYKPS
12060	25961	A	12170	260	375	EKVTCSWTQWLTPVIPALWEAKAGRSLE FRSLRSAAI
12061	25962	A	12171	304	3	KFFFFFFKGFFFLGGVGPIFPKKRFFS KIPPGVFFFPPLKKKIFFPFPVILGPP RVFFKGAPLEFFFFFFFFFFFSETEFRSC CPGRLECSVAVSAHCK
12062	25963	A	12172	105	3	LIFLRQSSALLPRLECNAGATSAHCNLC TGSSD
12063	25964	A	12173	146	17	RIFFFFFFLQSLAVAQAGVQQRDLGSLK APPPGVHAILLPQEY
12064	25965	A	12174	234	2	LFPRKPKPSVLSLSLSLFLRLRLKLS FMRHNNIEVRPINNPAMTSKCSERKSL VSFTLNLPKMIRLSEEGMLK
12065	25966	A	12175	292	380	VRGLGRVAHTCNPSTLGGQSGWITGGQE F
12066	25967	A	12176	109	1	GRIKKVIKQAQWLMPVIPALWEAKVGG SPKVRSSR
12067	25968	A	12177	170	291	LINFYFYFLRQSHSVTQTGVQWCNLGSL QPPPAARRRRRG
12068	25969	A	12178	260	380	LTYIALFI FLRRSLTLPRLECSGMISP HCNLCCLGSSDS
12069	25970	A	12179	54	166	PKRGFHRVTQEGLNLLTLGSPRLGLPKG WDHRQDPLP
12070	25971	A	12180	273	359	APAGHGGSCLOSQHFGRRLQADHLGSGV R
12071	25972	A	12181	27	225	IGQAQWLTPVILAFWEAKAGGSLEVRSS RPAWPIYFLVLLASYLRRFCLIQGHSDL LYTSSTRGS
12072	25973	A	12182	1	155	VHKIFIAKYSGFQTVFRGRAWLTPVI PALWEAKANRSPEVRSSRSRGRG
12073	25974	A	12183	91	2	FNLFFFFFFFETGSRVARLECNAGATSA C
12074	25975	A	12184	122	2	GQAQWLTPVIPPWEAKVGKSPPEVRSSR RTRGRTRGRTRG
12075	25976	A	12185	389	20	TDRGRRARRACFCGKVFDELSFALKLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REMGRPDWRAMLAGMSSTEYADWHRFYS THYFHDVLDMHFSGLTVTLSLFFSDP DMHPLDFSLNRRREADDEPEDDVLQMKA AGLAGGVFLI
12076	25977	A	12186	180	393	LNPGSGGCGEPRSRHCTLAWVTERESVS KNKIKIKINKQIEEGFLFPFGQGF IWC YFPAKEFI IALSKT
12077	25978	A	12187	37	443	PDFPIPFPPRKVQHLARPSPKTARPAWT IRRILPPPPKKRHPGGLARGKFGPRELA KAGLAKECPAGGPTPAVRPATPTRGGGG RVAGFQTPMGIPMGKARLGLLTFLGFAS GWIGAYRPRETLCGGELVDLTQF
12078	25979	A	12188	3	411	AFPENAAATGSTFQDFVPASKGRAEVDNM RLSVAAPISHGRVFRMRMLGPESRIHLL RNLLTGLVRHERIEAPWARVDEMRYAE KLIYYGKLGDTNQRAMRMADFWLTEKDL IPKLIVQLAPRYKDTGGPTRMLQ
12079	25980	A	12189	2	414	QEFGRTRKRTFISLFFSSVYSRGVFR RDAHKSEVAHRFKDLAETLRLALTLIAF AHYLHQCPFADHVKLGNEATEFAKTCVA DESAENCDKSLHTLFGDKLCTDAPLRET YGEADCCAKQEPERNECLLQHKDD
12080	25981	A	12191	3	514	PRLLMEAGPHPRPGHCKPGGRDLMNHG FVHHIRRNQIARDDYDKVKQAAKEKVR RRHTPAPTRPRKPDQLQVYLRHRDVS AHPRNPDIYESGESSSSSGSELEPSGHQLF CLEYEADSGEVTSVIVYQGD DPGKVSEK VSAHTPLDPPMREALKLRIQEEI AKRQS QH
12081	25982	A	12192	182	3	RGLFFI PPPPIKTKIWGPFWKVVFMGFG PPLFFFFFEMESRSVAQAGVQWHDLSLQ ALP
12082	25983	A	12193	53	400	PETPSWLGPVRRFYFIIKSVWKWKKKK KKKKKKKKKKKKGGGPPKKTGLGDKFYW GVKKKI FFFLGGSKKHPWGFF EKLF FGGKCGAPPKDISCLWGKKNFLGAIGEK TCCC
12083	25984	A	12194	182	3	KGIFIQIAPPKKKKNWGPLWKVVFKGFG HPIFFFFFEMESRSVAQAGVQWHDLSLQ ALP
12084	25985	A	12195	200	378	KSSKSQWLGYLFIGLLIYLFIFKFFLETR SCFVTQAGILAHCNLKLGSDDPPTSAS QAA
12085	25986	A	12196	341	54	SLSFHGGLSVLCIFSTYKKLSQEQWLTP VISVLWEVKVSRSPQVRSLRPGDPPASA SQSAGITGVSHHARPHLSLNPRLMIKL SEEGMLKRMTG
12086	25987	A	12197	1	462	GGPPRPFRMKA AVLTLAVLFLTGSQARH FWHQDEPPQSPWDRVMDLATAYVDGLKD SGRDYASQFEGYALGKQLNMLLDNWD S VTYTFSKLREQLGPVTQEFWDNLDKETE GLTHEMSKDLEDVNAKVQTYLYDFQKTW QKELTFTAESVPV
12087	25988	A	12198	80	1	SNKVFFLETESCSVAQAGVQWCDLGS
12088	25989	A	12199	221	3	TMGIMLDKKEIQAI FSKFKMGHAVAET TCNINNTSGPGTANKVTVQWWFKKFC KGDESLEDEHHGRRLEV
12089	25990	A	12200	239	336	FGALPITTCFKGKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKKKK
12090	25991	A	12201	279	366	KKKKKKKKKKKKKKKKKKKKKKKKGFK
12091	25992	A	12202	153	40	GFLFLIFFFFETKRSRTIIQAGVQWCHLGLCTLAWATETD
12092	25993	A	12203	317	406	LGKLCNGAVSGHCNLRPLPGSSDFSGSAS
12093	25994	A	12204	2	925	RSGPDHELTLDGKGGCTRSMPVPSAASEDRRLPIIIVEDEGGPTRSRACSSPARGSRPPPSAIGCSPVAQASDSAAGPARRTALQSLSSWLGYQIDRHSPVYVFKSPFLFSVIMAPKKHSSDAGNLDPRKRSRKVLPFSEKVKVLDLIRKDKKSYAEVAKIYGKNESSIREIVKKEKEIRASFVSPPTAKVTATVRDKCLVKMEQALHLWVEEMNRKRVPIDNSMLRQKALSLEYQDFSKGCSETDTKPFASKGWLHRFRHRFSHHYKKKKKGIMAQVAVSTLPVEEESSETRMVVTFLVSALESEM
12094	25995	A	12205	272	1	KMARAGLLVIEGKVWRTVYYRFATREEREGKSTNLNKLDTIGFDNKKDLLISVGLDVRGAENVECLELITFPWFRAVRGNHERQPGQ
12095	25996	A	12206	166	478	ISASGLLPTSPLTGTSTKLQDPNEHLNLLMLNRVSLLLPRLECNDTILAHYNLRLPSSNSPDSAFQVAGITESFTCEINALKDSQVALWSFRCEMDHSSICNR
12096	25997	A	12207	102	497	PLLLALLFGSQKTFCLQLSLKPTRSSLLSPGSAGNPENEAPCPQLNPEATSLKKKKKKKKKKKKKKKKKKKKKKARG
12097	25998	A	12208	131	2	FGFLGGDKAKGKGGPPPPFFFFFETESPSVAKAGVQWCGLGSLH
12098	25999	A	12209	221	499	QTRHKLTNSRSRGRTGLQILIKEQHSSGRWCGTFDILWQSLDITICYSVPKSLDLFLFIYFETESHFVTRLECSGAISAHCNLRLLGSSDSPA
12099	26000	A	12210	297	398	HNFFFFLKTESCSISQAGGHWYDLSSQPPPPG
12100	26001	A	12211	341	452	NWSPGLKQSSRLSLPKCWDRREPPCLA GLLAYLFRR
12101	26002	A	12213	214	468	FFFFFFWGKGVFPPPLEBGRGGNSVYWTTPPRGKKNFPPLGLGKMGNNPPPPPPRFFFFFFFKKGVFGLPGGVKTPSLRETPP
12102	26003	A	12214	223	477	CPTETQLQLIFAREKHKFSPVLLDLDLYGFFFMESHVSFLECSGPISAQSNLYL LGSHNSPA
12103	26004	A	12215	263	55	TPKRYGKMQTATYLPKSKTYIIISDLRKQDYIVYKQSKKPEGWAQWLTVPVIPALWEAKAGRSPKVRSSR
12104	26005	A	12216	328	471	GVTHAQVLHAHTHTHTCTHTQVHAHS
12105	26006	A	12217	434	1	WDHSASPPTS SVGTPLRADGPHPRLTABGHVVGSSAMLSAPAAGRRGLSLGRWC DRDKLSQRGPQPKWILWWGNLPGGGFLHRHIHKPLPTIPI PSTVRGEEVLQQLLHSASFILFIFIFLDRVSLCHPGWSAVERSFTTTSTST
12106	26007	A	12218	304	43	EKPIGVAPSRVKKRAGGGEKTECCLLKGPLQGFQGV LKGPLKLNGLPFFFFFLRRSLALFRLECNGTILAYCNCLLGSSDSPA



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SEI
12107	26008	A	12219	171	365	ALVQPRAGREAVTPACCSCSDVFLYET NKVARIQSINYGTIKFFHVIVFSYSKE HLKRKLEK
12108	26009	A	12220	171	452	ARYKFLHPKFAFGLYPSSSQIQGARHQL WILIKCSFYLLFLRQCLTLLPQLECSNM ITAPLQPQLPGLKQSSHLSLPSSWDYRH EFP
12109	26010	A	12221	323	458	FRVQRSFLFLFIYFFETESHVQAGVQW HDFGSLHRISP
12110	26011	A	12222	189	56	DRVSLVQPTLECSGTISVYCSLNLGSS DPPTSASPVASTTGGI
12111	26012	A	12223	246	494	FLCSSYAYDDHFLRPFPIHLILDITAF SQDTIISNLLFQDACSVPKAANLGOAQ WLAPVIPVLWEAEVGRLLLEVRSRPW
12112	26013	A	12224	55	353	RIQGCSCWVKLCPKVEKVVQRTDAEQES QTKAEIQDMKQELSAVNMDKFARSARL ERKINKMMNKLKTHVKVQTAQSGMLKWV ISVAFYKLPGTIVRL
12113	26014	A	12225	199	23	LKLSSIIYVPGTILKYFTGWARWLLPVI PALWEAEVGGSPVRRSRPANSTSWIER HQ
12114	26015	A	12226	369	14	DCVRVGLSYPQTVCPSCESVRKAPFSSR PHRGVLESGQPRCKSRVDIFFSMERER DRERERERERERERGQKTRRVWGGERE KLGYSWAWGRGGRGLWGGMCGIPPPC TSDVHQ
12115	26016	A	12227	206	2	QNGHMNGGPCRVLSLFLFETRSFLFFLA SLSMLECSGAILAHCNLRPGSSNSPAS ASQVAGITGACH
12116	26017	A	12228	231	501	RSWEGQALHGSDPLASCTRIQSNYMALQ RINQELEDKLYRMGQHYEBEKRALSHEI VALNSHLLAEKVTIDKLSEDNVSAHTW PMEDCR
12117	26018	A	12229	86	455	DLPTFPVPPHFGSGPLLGQSELPSNCQ TGRSHLSVSVLCPTLATPLGLDFPTC GTSQLPLGLQLAHRSELAGLSPLGLST NCTSQRLPDRPHRHSAPHTHTHTQHT HTHTHTPATVT
12118	26019	A	12231	211	96	KSHFKAGGGPPRYSPFPGGGGGVFRV GGFPPPGLTQ
12119	26020	A	12232	228	3	KRWFIKGLSKGLGPPPKLKLGLGFFFF FFFEQSFVLVAQAGVQLECSGTILVHFN LYLPGSSNYPASASHPRV
12120	26021	A	12234	137	3	VPLPGTLKNHSMVPCFLFVCLFVCYETE SHSVAQAECGSAISAH
12121	26022	A	12235	139	1	FKLCFGQAWFKPIIPALWETDASRSLE VRSSRPADAWADAWADAW
12122	26023	A	12236	80	1	VLLIFIFLEEMGFHHVQDGLDLLTL
12123	26024	A	12237	187	494	TERNSFNINKKDIHTKTFVGVQHQRPK VDKTTKMGQRNQRKAENSKNSTSSPPK DRSSLPATEQSWTENDFDELTEVGFRRS AITNFSELKEHVLTRTE
12124	26025	A	12238	252	503	CQGVGADDLQSQAEIQELCAESIDRFD ILFFFFLGLGPPHKNPPPTPQKWKPGK APPLALWDIPRGAKGPRQPRPAIHTC
12125	26026	A	12239	2	471	RIALCPAVRIRHEERERERERERETP GHTQLSPGARRTPLERERAFNDCPSLN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YPGNLCPGDLIEVFRSVYQHICALYLGDG YFINITPVYGIAPFFTSKSVFFSRALE KTHLLKDVVGSDTYRINYICYETLPSLS VEEIIITRSEFVIGQEA
12126	26027	A	12240	14	149	FMTACRIRHEMGRGLRLGLWPLHIVLWT RIASTIPPHVQKSALPH
12127	26028	A	12241	588	671	RSRPSFQEQAFESSQKYKEGKYIIELNH
12128	26029	A	12242	384	464	RGGQVWVWKPVVPALWEAKAGRSLEAG
12129	26030	A	12243	325	459	TYLFIYLFYFETESCSVAQAGVQWRDL VSLQPLPNSPALPTN
12130	26031	A	12244	323	457	SLQRECGPADTFFEMDSCSVAQAGVRWC DLGSLQNSP
12131	26032	A	12245	241	466	GALFFFFFFFFFFFFFFFFFLSNKAVY F
12132	26033	A	12246	385	37	QARRRCLQTSRMEALGRWSYKVTIEFPL QILFFPPIIKYKVIIFGIKITPNPHFLEE YEEGQRLGKSTVSWVFNEDTRLINIWNR HITVNPRTNSQNRMLMAHESKYSQVPP PLQA
12133	26034	A	12247	318	456	LILKYFMYVCMYVHMYVCMYIKSCSVAQ DGVQWYDLGSLQPPPPGL
12134	26035	A	12248	362	473	SPCQNNMNSAKTEARTNIKFMAKLMWKN GAIIDALQK
12135	26036	A	12249	310	463	FSIKTRKNALGKLQSLRCHQFYLYVCV CVCVCVCVCVCTRTYAILTCIAV
12136	26037	A	12250	169	54	EAKSGQARWLTLPALWKAAGGCPEV RSSRLAWPIW
12137	26038	A	12251	49	449	GIPATSTSCVQVILLPQPPLLLGLQDSF LPQEIIIKVEGEDTGSLTIPSGEIVNFK IVTVDFTREEQGTCPAORTLDRDVILE NHRDLVSWDLATAVGKKDSTSKQRIFDE EPANGVKIERFTRDDPWSSC
12138	26039	A	12252	130	428	RWGLAMLPRVLVNSWSQVILPQPQVGA TFGGFPNPPGHWKLGGISSGEEAGVEE ABEGQALGFLGQFPSPQLLLQTSWCL RTTRTCRWSLWKAH
12139	26040	A	12253	204	54	PGMHKTQKSDLGQVQWLTPVILGLWETE AGDSPESRSPAPAWAKHKIVR
12140	26041	A	12254	375	470	SLCLFFSFFFQTEPRCVAQAGVQWRHLS SLQP
12141	26042	A	12255	432	512	GQVRWLTPVIPALWEAEGGRSPPEARSS
12142	26043	A	12256	232	1	KGALSKKTQSFWGGQKFFPRPGVFKGVF FWGGGFCFFVFGGFFFFFFFFFETESCSV AQAGVQWCSLGLSLQLPPLPRFK
12143	26044	A	12257	22	123	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSSTRP
12144	26045	A	12258	71	362	QTERNSISINKDVHTETPSKGHQHQRFP KVDKSTKMRKKQRKKAENSKNQNASPP KDHNSLPAREQNWTENEDELTEIDFRF WVITNSSELKEHV
12145	26046	A	12259	375	3	SPNIEAPPKAAFFFNQRHFVFCFFSCRA ENTHEIVVVKVYFNSQSKALFFSFFV QRDRSSPDSYLMPLQLQMWDTAGQERFR SIAQSYYSANALILAYGITCEESFRCL PEWLRQIEQYA
12146	26047	A	12260	98	1	KYQIDLGGRGSSNSPASASRVAGITGTH HHTQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12147	26048	A	12261	125	3	LFLIQKYITGQERWLTTPVIPAPWEAEAGRSPKVRSSSPA
12148	26049	A	12262	228	385	SCLYLQMIPTSSIEKSQGMKKATRGRARWLTPVIPALWEAGAGRSPEVRSSR
12149	26050	A	12263	227	369	MLKHKSNNKLDLQGMQGLTPVNPVLWEAKVGGSPDEVKNSRPAWPTW
12150	26051	A	12264	102	487	QQNRFFGTERGRGTGRGVSSFPQLSPGSLLEASSPSPSVGRLGSAASQSRSGGQERPKAQLRRPPRPSSSPRLRGRENCAHHARTPGGILDRPPTLTGTNLLKGGRPAAWMAGNPPEAHKTANGPGEQA
12151	26052	A	12265	391	476	PRSYRVECSGISAHCNLGLLGSSNPSS
12152	26053	A	12266	378	476	MSSRLGSLLEVIGILGRAWWLTTPVIPALWEAKEGG
12153	26054	A	12267	166	58	NFFFFFFFFETDSCSVAQAGVQWHDLSHCNLCLPASSN
12154	26055	A	12268	209	49	TPPNFYIKISRSQQAWLTTPVIPALWEAEAGRSPEVRSSRPASPTRNSISNS
12155	26056	A	12269	127	1	SSSFFFLKTFGLFFFLCFFFESESRVAQAGVQWCHLGSLQA
12156	26057	A	12270	154	27	IQTPGKKEFFFFFFFFETKSCSLVAQAGARLCPKKKEKENSNFVL
12157	26058	A	12271	180	22	VLKIHNIQRAQWVTSVIPELWEVKAGGSQALRSSRAARTRWDACNFVEKTQVY
12158	26059	A	12272	207	422	GDSSTRGADEKPKKEGVKTDNNNLINLKVMGQDCSMEQFKIKSHIPAGYGGSHRESQHFVMPRWADHLRSGV
12159	26060	A	12273	59	479	NSLGGGGVYGSRRFTFPGCRALSPWRVRVQRRRCCEMSTMFADTLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGRQKKKIERQEEKLKNNNRDLMSVVRMKSMAIGCFCTALMGM
12160	26061	A	12274	354	439	VKTGECSTAKTWNQPKCPTTIDWIKMW
12161	26062	A	12275	366	499	TRAQYFVVVVGIGSQCVTLECSGMIMAHCSLDLLGSSDPPTSAS
12162	26063	A	12276	136	37	KFPGQVHWLKPVIPALWEVKAGGSPEVRSSRPA
12163	26064	A	12277	419	48	DGKLVNSFLTSSSGCFLIFLLIVRPPYFLRYNNSEIRPINNPTMTCKCSSKRKSRICLTFNQKLEIIKLSEEGMSKIKTGQNLGILCHVSQVVDEQHKFVKATKSATAKINLSISKYIMSGA
12164	26065	A	12278	190	1	RKGVFSPQMGPGLGKSKSPFLAKLNFPFKKTFFFFFFFFETGSCFVAQAGMQWLDPSPPDAWADAW
12165	26066	A	12279	276	389	WFNLSFFCFCLFFETESCSVARLECSGAISAHCNLT
12166	26067	A	12280	425	1	PPHPPPGKPPPPPRPELFFPKTKNKKERVLFFSPPPKKNFFSLTTPRFFSPPQKKKKKLNPQQKGPVPIKPPPLFFFFFFFFFFFGLTVRVIMTCWLIVDIGLLI
12167	26068	A	12281	253	90	IWPPQGSFKTAAPFFFFFVFLVEMGFCHVVQAGVKLLTSSSPASASQAEKLF
12168	26069	A	12282	61	387	PKSSSSAPFQISSWFSLPASTSASTMSIRVTQQPYKVFNSGPAFSSSSYMSRPSAHISLIVSRVSSSSTSFQGGGLGAGMGLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LHSSLANRRLRSQKKKKRGGRSKEP
12169	26070	A	12283	186	305	LHSTVQVRREEHKSLSHTQVHTHTHTHT HPHLVIMSSHS
12170	26071	A	12284	2	190	PRVRFDRVNNRSLNPLISRTMTRIEPIPE NPKFSVKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKGGGA
12171	26072	A	12285	17	197	SLGVGGGQGGGGVHFHPCKPFIVLSPVS LSKHCSYLPKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKK
12172	26073	A	12286	158	405	GVASAEQRKYFLEMEYFPGGEAISTIVE MTEDLHYSINLDDKAPTGFERVYSHFE RTCTDDKMLSICYITCYREIFCERNKL
12173	26074	A	12287	364	142	GCAFFLGGPLKERRKRRVPPPLFFNFNF FETESCSVTQAGVQWCNLSGLQPLLDW WCQPGTVAHACHPGTLGG
12174	26075	A	12288	171	380	VFEAGHAWLQENLTSPDFWGFSPFPTDT GMLEKKKKKKKKKKKKKKKKKKKKDR
12175	26076	A	12289	194	2	GERGFQWQVTKGFFPKKGFVKFYPPAG GWFFFPKRGFPFSPFLFFFDVRVWLCHP GWISVARS
12176	26077	A	12290	179	416	LIFLFTFACAVCFQLARFHKIHIETAL RCLIIILSCPPTHPLYKMYREGQARWLTP VIPALWEAEVGGSPVEVRLRPAC
12177	26078	A	12291	3	408	LAYGFHRTTYDTTPSALMMVLLVDELIT GNKNGSGEAPYLPEDFRDGEDDAAVTL EKQEDLTTLVTLPTLGEHQQRQRETQLE AKLLKKRLELGLSLDLVDELIIQLKK KKKKKKSPWGAFFKGPLGAPI
12178	26079	A	12292	119	278	PKSIEAGVKSVDHPLPNKAKTHLSCKK LKKKKKKKKKKKKKKKKKKKKKKKKKK KKKK
12179	26080	A	12293	119	3	MLFTGFHTKVMSLNSTGWAWWFTPVIP ALWEAEVGS
12180	26081	A	12294	205	1	ILHFYSTETKQPKGLFLALFYSDCEQEK RKGGKLLKIFKKAQGOARWLTPVIPAFW EAKVGRSPEVGS
12181	26082	A	12295	215	1	AFKIKLTMHIFSSPLCLPQDEFHPFTEA LLPHVRAIATWFNLOARKRKYFKKHEK RMSKEFHGARLEGNO
12182	26083	A	12296	185	411	DVPLMFHWLHLHSDFRISTEIGVETVG KRVLHIRILLLLLLLFFEMESCSVTHAG VQWCDLGLQAPPPGFTPF
12183	26084	A	12297	281	388	RILFFFFFFETKFCVSPQAGVQGRDLNSL QPPPPGFM
12184	26085	A	12298	178	3	TLLSVTQVPILPGSASSPLLFSSRKDIKI PTSVFFSFQTEPRSVTQAGVSWCDLGLS QP
12185	26086	A	12299	199	450	TLIRHMICNYFLLSHRSFPSSVDYFLCY REIYSLIKTLNKLIGGFFLNIIKVMYD KPAASIIRSSEKQKAFPLRSCTRIRCP
12186	26087	A	12300	3	407	EFKDHSTAMDTEPNPGTSSVSTTTSTTT TTTITSSSRMQQPQISVYSGSDRHAVQ VIQQALHRPPSSAAQYLQQMYAAQQQHL MLHTAALQQQHLSSSLQSLAAVQASLS SGRPSTSPGTSVTQSSMVQTSI
12187	26088	A	12301	227	3	KRGTEGQTLFFPAPRARKSFPPPKMPKK VEKEFPKGFFFFFFFFFETESAPSPRLCS GAISAHCSLNPHASAHAS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12188	26089	A	12302	292	380	KCYRWARWLMPVIPALWEAKAGGSLEPRN
12189	26090	A	12303	13	186	VDERHIRLSEMAWVALYLLSLLWATAGTSTQTQSSCCEYDVFPRRSGKQLPWGRGCDL
12190	26091	A	12304	253	409	ITAVIAAAAAVGVVTIIMTNFRSLPRLECNGATSAHRNLLLGSSDSPASAS
12191	26092	A	12305	153	64	GRAQWLMPITIPALWEAKAGGPLDVRSSRPA
12192	26093	A	12306	265	420	GTLMSRNTKLQLCRMNKSRTLQGPWWLT PVIPTLWEAKAGGSLEARCSRPAW
12193	26094	A	12307	295	1	RPCLKNKKTSPHWKKKFANPLFGKAPVFLDKKPFKPHYRESRPLKKKNGPKGFF FFFFETESCSVTQAEVQWRDLGSLQAPP PGSYHSPSKLI IKN
12194	26095	A	12308	247	421	SWCCLKKKKKKKKKKKKKKKKKKKKKK PGGGALKKKKIF S
12195	26096	A	12309	168	3	GQALLLLCLTVAFSKTTVVCHAPILGWA WWLTPVIPALWEAEVGRSPEVRRSRP
12196	26097	A	12310	117	3	VAYNIAVFRGGVSLLLPRLECSGVISAH CNLR L P C S S
12197	26098	A	12311	256	101	EPPTFFFFFETGSCSITQAGQRRDHSP PQSPTPGLSNT PAPASRACESGR
12198	26099	A	12312	146	3	FVALCQLFPLVNVICFHKKHKTGRARW LMPVIPALWEAKAGGSPEV
12199	26100	A	12313	207	3	VRVRTTGVIMALRGLCFSVESMTKDEL IARLSLGEQLNRDVS LTGTKEELALRV AELQELDDSR
12200	26101	A	12314	282	2	NCLAEKVVKFMVSAISLQPPGISILFLSF FFEKESCSVPQARVQWPNFSS LQSPPPGFKLFFCLSPGGGCSEPKSCRCIPGWQQ NETPSQKKK
12201	26102	A	12315	298	84	KTPQPPVFALSKNFGPPKTAPIFFFFFF FETKSYSVAQAGVQWRDLGSLHSSLGHR ARLHLKKRKRKSNL
12202	26103	A	12316	124	1	SKGHFFFFFFFSETESCSVAQAGVQWHNL GSLQVPPPRFTPF
12203	26104	A	12317	132	398	VVTNAVFSIVTFSPSVCHSEVALAAYKW LVCYLLRETYQLNQEIKP TLSPVKKK KKKKKKKKKKKKKKKDKKK
12204	26105	A	12318	262	392	PHYCQNQPQARRSGSHQHFQKQRRREDHL SLGVRDQPGQYSETP
12205	26106	A	12319	168	3	EAPKATSNCTTALQPR LQCKNLSQNKEG QVQC LTPVIPALWEAKVGSP EVRSS
12206	26107	A	12320	48	385	DLGLSGHSTLASSFISL LLSYK KCLSP STMIMRLPLPCGSP I KPFPLPKKKKKKK KKKKKKKKKKKKKKTGG
12207	26108	A	12321	218	83	NLSPIFPEGNFFFFFFFEMESRSVAQATV QWRDLGSLQAPPPRRKF
12208	26109	A	12322	197	1	KETWFPFPKKEQGLFSFFKKRIFFFFFSK KIPSPFFFFFFFETESCSVAQAGVQWH DLGSLQAPP
12209	26110	A	12323	128	36	KGLFFFFEMGVSL LPRLECSGTTSAHCN LP
12210	26111	A	12324	140	3	ILNSNLKPIKNTFF FETESRSIAQAGV QWHDPSSKQPPPLGFKR
12211	26112	A	12325	273	369	RKEWFLKKKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKK
12212	26113	A	12326	140	415	RTGLLGPGRLLQGPYPYGSREYKSGLLDL NASLLDPEVWAPSLSGPETKPPAHSPSD PGVHSSCSASQGSQGPPLTPSSRIHEP KPPGPFCK
12213	26114	A	12327	2	506	FVPLSETEAPGCSGSRPPELEPERSLGR FRGRFEDKDEQLEEEEELEEEEEEEEEED MSHFSLRLEGGQDSEDEERLINLSEL TPYILCSICKGYLIDATTITECLHTFCK SCIVRHFYYSNRCPKCNIVVHQTPQLYN IRLDRQLQDIVYKLVINLEEREKKQMHD
12214	26115	A	12328	1	419	FRVPSCARCQYLPLLRGASQLGYSVGRD PVEEAVCPFSDLLKLCAGRTTTLFKAVRQ GHLSLQRFLLPFVWLCAPARSGVYRGRQ ASLSCGGLHPVGASWPRCLPTQASAMAG TPPPASLPPCSLISDCCASNERGSMGV
12215	26116	A	12329	259	414	NMENSLRCVWVVKLAFVLFASLLSAHL QVTGFQIKAFALRFLSEPSDAVT
12216	26117	A	12330	302	404	SCYRVSVISQARWLTPVIPALWEAEVGR IPEVGS
12217	26118	A	12331	94	375	SRDMSPGLLTTRKEALMAFRDVAFAFTQ KEWKLLSSAQRTLYREVMLENYSHLVSL GIAFSKPKLIEQLEQGDEPWRENEHLL DLCPGWSAMA
12218	26119	A	12332	7	246	NPIVDPSPCGGIRVTPAGRGGPALVRV PETWEEAGEKMPSESLCLAAQARLDSKW LKTDIQCFTIRKISLLPLFCHHL
12219	26120	A	12333	150	1	YIYFFHLVRGLPGSGYDEYFVVVVVNTS SPSVTQAGVQWCHVVSQHKPP
12220	26121	A	12334	34	426	BPGFLFVFFLIRGKKTPLFFWGTRKNP KSGKPLFTPPGKSPSEPPKSRGGPLFFQ TRSRLTPQSWFGGAPKPLGGEPPKFEW AGLGGDPPTPRAPHRADQTLQPIQAPT RLIQNEQWAIKPFQPMPPG
12221	26122	A	12335	185	3	TVITPLHFSLGHRARLWSRVPAPPAENR SMEGGLGRAVCLLTGASRGFGRTLAPLL ASHE
12222	26123	A	12336	60	316	GWGPIPSTDVTVLSPQKPILLQGERAI TQIKYNREGDLLFTVAKDPVSVGWGSG RGGILLPGRWVDTPVLPFLAGNQASHCE K
12223	26124	A	12337	3	167	SFRIQVQGNHTSKHYPKIQYSDQAQWLT SVIPALWEAKTGRSLEVRSLRAFRAP
12224	26125	A	12338	238	401	RPLSVMCGRLTSIRVEDSGARCWFYLF IYETEFRSVAQAGVRRDLGSLQTPPSG
12225	26126	A	12339	354	433	GWAQWFMPVIPALWEAKAGVSPEVRS
12226	26127	A	12340	238	382	LLIVYNMMLLPDAVAFTCNSSSTLGQGR RITRGQEFETSLANMVKPHL
12227	26128	A	12341	101	1	KTQTNKKTRSVGQTWTFPIIPAYWEA QAGEL
12228	26129	A	12342	276	23	GSCLEGLTNRKDIHTKTPSVRHHQR PKIDKTTKMGRNQSRKAENSKNQSSSP SKECSSLAATEQSWMPHDFDELREGEFR
12229	26130	A	12343	122	1	YMGVNERGCGQSIFKSSSLSSQLWWAF IIPATQEAEGEW
12230	26131	A	12344	180	360	LHVVFYFVSGDFLPPPPPLDDSSALPS ISGNFPPPPPLDEEAFKVQVRAEVKVML GKS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12231	26132	A	12345	35	411	TMTIVDKASESSDPSAYQNQPGSSEAVS PGDMDAGSASWGAVSSINDVSNHTLSLG PVPGAVVYSSSSVPDKSKPSQKDQALG DGIAPPQKVLFPSEKICLKWQQTHRPGA GLQNLGNTCFANA
12232	26133	A	12346	278	386	ITICYKQTTIGQARWLTTLIPSLWEAKV GGSPEVRS
12233	26134	A	12347	111	2	KSQTGQVQWLTPVIPALWEAEVGGLEL RSSRLAWA
12234	26135	A	12348	215	316	LNKRLMISFIKKKKKKKKKKKKKKKKKK KKKKKKKGGPL
12235	26136	A	12349	265	404	SNISYFLNNNFSKALSNIKYMISQARW LTPVIPALWEAKVGGLE
12236	26137	A	12350	372	1	PVFPLPPKKLGEQLPPPALRFLAVSPLP KAAHEQEIKEKVLAVHKNPIDPVYGFPK KGPTNFFLPLFQRVIFLGAQKGVSWFG FYVKGLSLAPKLGGPPFFFFFETESRSV AQDGVQWCDLGS
12237	26138	A	12351	318	416	QGRAQWLTPVILTTLWEAKAGGSSEVRSS RPAPP
12238	26139	A	12352	144	1	NGYAIVECVLFCFVFLRQSLSVAQAG VQWCNLGSMQPPSTSLVQAI
12239	26140	A	12353	116	1	SGRYSFKMKCKGQERWLASVIPALWEAE VGRSPEVRS
12240	26141	A	12354	102	2	ETRYKKQPGCWERWLTPIIPVLWEAEVG GSPEV
12241	26142	A	12355	112	294	LISPCPMWPSPHGPTWLSRLISQHS NLKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKRGGA
12242	26143	A	12356	138	2	SFFLKVFFFFFFFEMESRSVAQAGVQWCN LGSPQAPPGRHCPVD
12243	26144	A	12357	148	394	PGEPPGEKGGGKGGKPGGRGWGEPPCR GGFKEKFPRGKEKAPPLKENSRENLGW TKIPPLGKKKPPPPQEQEMILGPPQF
12244	26145	A	12358	97	3	EKFSPCFVRARHTHTHTHTHTLSLSLF GFH
12245	26146	A	12359	204	2	KHYTPAACFAPCLPDEAPIIAAAKPATT TSEQKMAVPPKYANLGKSARNVFNKGYG YGLINLLKTKS
12246	26147	A	12360	156	391	NRGLFKVEESFSPICSVRCSIHPSALVS PTPPTDITTNWALFFETESCSIHQTGMR WRDLNLLQPLPPGFKRFSCLNL
12247	26148	A	12361	179	1	ALKKLLIIDDNSHKTNIKHFSPFRNFTF LFLLTESRSIARLECSANPTHCLNRL SGP
12248	26149	A	12362	218	391	TILKDCFTKMICLSQAQWHIPVVPATWE AESRGLEPTS
12249	26150	A	12363	2	356	TNSHVDNSITQKPEFCIPRCCGYIVCQL QLVERAFIFNFFFFFFLKRFSVLLPRLEG RGAI FRVTQEGSNLLTLGPAPLGLPKGW NYRGDHPGPAYFYFLMGKRLQLIQGGRG LKRNL
12250	26151	A	12364	94	1	KNPPLFFFFFFFESESCYVAQTAVQWHD LGL
12251	26152	A	12365	237	2	YSSLLFKPAESAKGILRHHVTPKSTSAI SKILFCFLFFVETFLSPGLKCSGAIKV HCSNLGSGSSNSPTASQVPGS
12252	26153	A	12366	340	442	GLFVCFVWFLETESCSVTQAGVHWCDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSLQPS
12253	26154	A	12367	208	45	EGGEFFFFFVSFFFFVRAGVLPCCPGWS ETPGSSDPPALASQSAGITGATVNST
12254	26155	A	12368	60	443	CSSCVSSKQSPHLKKQGRMGHLSG GCTEATAGKMRKCLVAWSTCAGARPPS RNRGSQGHSAFQGPRLPTVVRLPPPP QAKPFCKKWLGGPISIEPKQHPGPG KKKWAGKAAPRLVPT
12255	26156	A	12370	341	421	SGWVRWLTPTVPALWEAEAGGSPEVGR
12256	26157	A	12371	280	393	NTIDHYVTQWLTPVIRTLWEAEAGRSPE VRSSRSAPWT
12257	26158	A	12372	268	399	TLCSLSSAESIIHSYPFESCKDNYLMTH NEAYKACMRRAFHIP
12258	26159	A	12373	209	468	EAVPDETSHPSPADSFTSSNLACGTHH LRRLKLKYVEEELEYPRKIQCFFHSFF FFESRSLLLPRLECSGISAHCNLCLL GS
12259	26160	A	12374	381	488	TITCLFQKCQRGRARWLTVPVIALWEAE AGGSQGE
12260	26161	A	12375	276	395	GHVVKTKKLKLIFFVFEMESCSVAQAGV QWHDLGSLQPPP
12261	26162	A	12376	295	472	VYSSVALNTFTLLCNHHQPSPEVLTFP NKKCRGAILAHCNLHLLGSSDSPTSASR VAG
12262	26163	A	12377	390	511	PGAVAHACNPSTLGGRRGGQITRIPSL
12263	26164	A	12378	417	511	AHRSFFEMESCSVTQAGVQWRRLGSLQP SPP
12264	26165	A	12379	133	406	KLSLNKRDKYKQVCKETKKKKKKKKKK KKKKKKPGAKKKKSGGSPR
12265	26166	A	12380	247	345	HMWSSQLNKGLINKKKKKKKKKKKKK KKKKKKKKG
12266	26167	A	12381	156	15	NFFFFETESCSVTQTRVQWFDLGSLQP GKQEQNYVSKNKQKELIH
12267	26168	A	12382	275	1	KIVFLKGPPPLFFFKKFVFFLKVGFKG GLNFIKTFFPGGKPISKKRQIFFFFFFF ETEPHSVARLECSGTISPHCNLHLPSSN DSLASTS
12268	26169	A	12383	43	379	LLGYDESRSLSWICLCLSLGQLLSFLN LLVYVFCQTCEVCFHYFFQYFSTLFLLT FWDNSVLNIRHFGIVPQVLDLVLFFSPN KEIFLGQLQWLMPVIPAFWEPEAGRSPE
12269	26170	A	12384	303	1	KGFFFFFFGLSPFFFLKKVFFPPFFLRT PPFFFFFFPFFKNFFPPPPKKKNPPFFFP PPPPPPPPFFETRSRVAQARMQWGD HGSPQPQPPGSSDPTRP
12270	26171	A	12385	141	1	KKEPLRAPPPQLFCFFYFETTPCSVTQ ARVQWCNLSLQPPPLRYK
12271	26172	A	12386	31	417	CRLADSPSPNDTGQDSRGRAGIKHIPPL KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKSGGA
12272	26173	A	12387	291	412	LSSEMLLCFVYFLRWSFTFVAQAGVQW CDLGLLQPLPG
12273	26174	A	12388	310	1	MTPCPFLFFCPKKRAGGGFIKKALFFN PQKEVFLGPPPKGPFLLGFQPTPPWGKK IPRLNPLFWRSSIFFFLDGVSRLPR LECNGLISAHCNLRLLGSS
12274	26175	A	12389	117	2	KRNPQRGGPLFFFFFFFETESRSVQAG



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AQWHDLGSLQ
12275	26176	A	12390	117	319	SFLKKPKDSTKNLKLINFEFSKSGSPKI TIQKSVAFIYPNGEHSEKKIREVITFTI AAKTIKCPPQA
12276	26177	A	12391	95	2	SKSWTSLKLRTLGLWARWLTVPVLPALWEA KAG
12277	26178	A	12393	127	395	IPGSQGFCLIKQSALHLLNKSSFSFLSF IETQSLSVTQAGVQWCYLSSLQPPPPRF KLROKNRLNSGGRGCNKLRAHYTPGWV TERDS
12278	26179	A	12394	252	391	FFCFCFVLLCFEMESCSVAQAGLQWPG LGSLRQGFAMLARLVSS
12279	26180	A	12395	275	3	TFRVLILKKSKETVEINCLETKSHSVAR AGVQWCSQDWEEKAGFNWRPSKARRCP TSVLKCHLGWAQWLMVPVLPALWEAKAGG SPEVRS
12280	26181	A	12396	111	3	GNNVKIRGLRIRPLKGWACWFTVPVPAF WEAEAGG
12281	26182	A	12397	124	1	VSRGRTVHQEKPTERAASPRLECNGTIS AHHNLCPLGSSNS
12282	26183	A	12398	259	387	YQQESFSCLFIFIFLFFIFYDTESRSVA QAGMQWHDLGSLKPP
12283	26184	A	12399	103	1	KGRFFFFFFFFYETESRSVAQAGVQWRDL SLQAPP
12284	26185	A	12400	308	416	CGNNEKAGRVRWLTVPVLPALWEAKAGG SLEVRSLR
12285	26186	A	12401	92	1	HTWGLTQWLMVPVLPALQEAQVKGKLFEP SS
12286	26187	A	12402	265	388	GLSWLFRPRGHLFYFIFPETMSVSITQA GVGCCDLGSLQPP
12287	26188	A	12403	279	1	SLSSKMESGSLTFSTIDIWGIITLSCC PGHCRMFSIRGLYPLDASSTTSSSCNN QNSPDMGTCSLWSQLLRRLRWEDCLNTG GRGCSEPGS
12288	26189	A	12404	387	152	NPPPGFNFGGPLKKNFFSPPRGEKFVFL KRPPPPPPPPPPPPPPPPPPPPPPPPPP RDLGSLQALKSFCDLVSAFKGF
12289	26190	A	12405	262	464	IIFHWLACILVIHSSFDGHGLFLPLAVA DSAAVKHSCSTICLNIEYIPGNGIAGSC GISVLNFLRNC
12290	26191	A	12406	204	67	KCFGQAWWLMVPVLPALWEAEAGRSQELR SSRPAAWAKELLNNRTRAS
12291	26192	A	12407	134	1	IQRPCIQLFSTFFLILFYFIFTEIDSCS VAQAEVQWHDGSLQPP
12292	26193	A	12408	145	403	TYMYSLINYKANSHTVKNKHNTARFL ESLLCAHPNPPIKLIISLLREKKKKKK KKKKKKKKKKKKKKQK
12293	26194	A	12409	65	415	RNKRIISQSWNGPSRKPSALLCGLGH LTSGVRRVSPVQGCVRKGGSGPSKP KKKKKKKKKKKKKKKKKKKKKKKQKGG ALKKK
12294	26195	A	12410	124	404	PWWEFLHHRNCQMWPGTVAHTCNPGLG KKKKKKKKKKKKKKKKKKKKSSSSSS
12295	26196	A	12411	164	2	TGAGLTIMDMVGVPDLLQLRFCVFLFC FLVFFFETESDSVAQAGVQWCNPSSL
12296	26197	A	12412	114	3	PGMVAHACNPSTLGGQGGWITRGQVYKT GLAKTVKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12297	26198	A	12413	583	391	LADTGFHHVQADLKPLTSCSTRLSLPK CWDYRCEPPLHLPVDPDTVLSTRGLISEKS FLPLCTFR
12298	26199	A	12414	280	2	KVSSMNAQTSVLFSTMLGISETLKYRGR KKRREREGREGGREGREKDECRKVRSER IEGGKKRGRKEYREEGRRRRIEVSANEET PRDHPANK
12299	26200	A	12415	264	352	RFLVHGCDIYICINIYTHTHTHSHTH T
12300	26201	A	12416	359	485	TDARMDWCYQEGTGSQAWLTPVIPAFW EAEAGGSFEVRSR
12301	26202	A	12417	171	1	PLFRWWGFELFPFFGYQKKKGYPFFFF ETEPCCVTQAGMQWYDLRSLQPPPPEFK R
12302	26203	A	12418	265	1	WHKSNEELAAEASAPVKARASNTILGPH THGKERCPVSLRNVLDEGVKSTNFFSFF ETDSHVTQAECGSAISAHCNLHLMGSR DSGA
12303	26204	A	12419	278	388	SSLTGFFIRRRNEEPGQHGETPCLLKIQ KLAGCGGVL
12304	26205	A	12420	205	413	WNLFVYLYQTHKYARVSYNIILFTNKK RAIGQAEWFTPIIPAVWEAKVSRLEPEVR SVRLSLPKWRITS
12305	26206	A	12421	103	2	RSLSKHRTETILGLPAAVLIILFPPLLI PTSKY
12306	26207	A	12422	372	478	NIFVFLKETPCQSQWLMSVIPTLWEAEA GGSLER
12307	26208	A	12423	174	416	KMHYCVLSAFLILHLDTVAILSTCSTL DMDQFMRKRIEAIHQILSKLKLTSPPK NYSEPEEVPPEVISIYNSTRDLLQE
12308	26209	A	12424	572	733	RFSCSLSPGSDYKNCNLSGSRGYSEPR SHHCIPAWVTEQDSVSKQNKTKQSA
12309	26210	A	12425	123	2	GYIFIFYFFETGSCSVAQAGVQWRNLG SLQLPPSSSDS
12310	26211	A	12426	224	417	TADFYGVNYISIKLLPKKKKRGPFKE SKFTAAGLQKNIFFLSAPNFIALAVVLK RRDWETPG
12311	26212	A	12427	115	3	FFETGSHPVTTQGMQWDCNSLQPLTNR LKQSSHLSL
12312	26213	A	12428	250	398	PWAGHLTSLGLSLPIFNIGIAGACWLM PVIPALWEAEAGRSLEVRSSK
12313	26214	A	12429	215	3	KKGLVVWGANKLWVFTPOKFFLNQFSGW ALTPRGKSWFSKRRAPAPFFFFFFWETE SHSVAEAGMQWHD
12314	26215	A	12430	345	2	FSHHPAKPQGGLFYRQPLGLEGKETRPR LNDRFMAGPSFPAQGLRMPFLGKEWER EGCSFVQCPVEGFAMWPYPLGSPGPRL FFFFFFEAGSPSVTQAECGSGSITANCSL EL
12315	26216	A	12431	348	3	LYSSLGDRVKLRLKTKTNKWCLHSYIS TCKIINLDHYLIPCTKTNSWIKYLNVR TNSIKLLEEDISVNLHELGSNDNSFLAMT PKAEIIKEKIYKLHFIKIKIFHVSIEDII EK
12316	26217	A	12432	160	52	NTAIGHPHQAIYLSYLSIYLSIYLSIY LSIYLSIYL
12317	26218	A	12433	180	2	GRSKLHCREHSICATEHVCGCDTENNT NLCQVQWLMPVILAIWEAEAWRSPEVRS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LRA
12318	26219	A	12434	193	3	PGAENPPPKGGPPFFFFPRGFPFGVFF LKKKGFPFFFFFDTESRSVAQAGVQW HDLGSLQ
12319	26220	A	12435	321	422	NVEGDFLQRIKNIRYWP GAVAHTCGPST LGGRGG
12320	26221	A	12436	116	2	HDRFCLFVYDRVSTLSRPLECSSAISAH CNLR LPGSSN
12321	26222	A	12437	302	400	THTHTHTHTHTHSGLLYLPKGKQSH EFCW
12322	26223	A	12438	329	399	LALQARLECNGIISAHCSLCLPY
12323	26224	A	12439	310	2	KPILSRGLFCARPCFRSNMRSFNPSQS YQVGKDTFGFTVKVTKLVLGPSRGPKG ARQGVHKGKCLLTLPKMLRFLFFETES CSVTRLECSGAILAHCNL
12324	26225	A	12440	151	401	EGMPHLPGSHSSSNILKRGRESGREAGR KGRKERRKEGRERRKEEEKRGRGKIRR RKDRGENEEENNRLSSKVSLEISTCP
12325	26226	A	12441	276	1	FHPFGRPSVSPRVQPKIGIIHTCVARI EKGGSCALSLCPQYVGSNFFFFETRS FSVAQAGVQRCDLGSMPHFPSSDPP APASRVAG
12326	26227	A	12442	140	1	NSHFPPKNLGSPSSFFFFYLETESRSVA QAGVQWLDLRSLQPPPPG
12327	26228	A	12443	310	3	LPPCSWGLYGAFARCP LMDKQLSQVPL WACPLSTAGRTRLCVACIKAAAGKAQGF FFFETESHSVTQAGVQWHDLSLQPPTH AKPKHTHTHTQTHTIPTD
12328	26229	A	12444	337	2	GFFAIVPKKGQKKMFSPFKEGIFSGPC FISSTPTLLGVKKILPNTSEIRPVLSS IINTSVHIREQKKTTVGIFTGKSRFFF FETDSRSIAQVGVRWRHLGSLQAPPPG
12329	26230	A	12445	112	9	GRVRWLT PAIPALWEAKAGRSPEVRNSR PAWPTR
12330	26231	A	12446	172	3	IPGELLIGRAKFAKNWPAPRGIPLGR QKFSFFFFFETESRSVAQAGMQWLNLS
12331	26232	A	12447	221	418	RKAERLEVFRRRLCQRALRPFPHCLAAA PMPLIVLKKPILGRAWLTVPVIALWEA EAGGWLESRS
12332	26233	A	12448	280	392	PLGRVRWLTTPVIAHWEALAGGSPEFRN LRPAWPDMA
12333	26234	A	12449	410	129	PSQEIFFYPGPPGKTPFPLKKKKIKNRGG GGGLPFPFPKVKKKKFYPGRGRFKQP KFNP LPPPRGEKKNPKPPPKKKKKEK KRKEKKLVT
12334	26235	A	12450	159	1	KKKRGGLGLTFIKKTGPDFFFFFETE SRSVAQAGVQWYDLGSLQAPPPGLM
12335	26236	A	12451	270	1	NPLKFFFSLFQNP LKKDPAIFNPFFFF FPRIFWPFFGGVSKAGIWWFFFFPFFFF FFFFFETESRSVAQAGVQWRDLGSLRT RGRTRG
12336	26237	A	12452	249	33	DKLVKLPLILKKLNSFFFFFETESRSVA QTGVQWRNLGSLHPPPGFKPNWAYAW AHAWVVPGLPAQNLR
12337	26238	A	12453	190	86	TNDLGWTQWLTPVIALWD A EAGRSLEL RSTRKA
12338	26239	A	12454	318	2	PPTFPLKTLFFPVFLPKLFSTLFSPPKKK FSNFLVSAPPPFFLT L GNSQGVLLKGGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						FFFFFFFFFETESRCVSQVGQWRDLEKK EKKKCNNGGRHYISTHLKYK
12339	26240	A	12455	204	288	IQLNTHTHTHTHTHTHTHTHNETGKMW I
12340	26241	A	12456	409	13	QGGAPPPIPIMLSFLQEAGLLHVAQPGVK LLTSGDPPSPPSKSAWRQQRTRNLGG RGRSEQRPPPRPPAWATQQDSVSKTNKQ TKNNKKIRKSLCKTLEKEMLAVMIITK YLLCTDVPSTVLCTHLYYLT
12341	26242	A	12457	204	3	KKKSPFPQSAKFPLGGGVFFFLVGMRS PFVAQAGFKPLGSSDPPILASQSTAITG MNHHTSSAFH
12342	26243	A	12458	289	3	KAREKKKVGATKNIRIVDLKSGRTSLCK KTEMPVGNRNKQKPNPSNLRISTRPE TESRSVTRLECSGAISAQVILPGSSDSP ASNWRQSETLS
12343	26244	A	12459	261	388	SWHFGRSKQVYCLSLGVRNQPGQNPVST KTKKISQAWWHAPW
12344	26245	A	12460	313	391	RVGRVHWLKPVIPALWEAVAGGSPEV
12345	26246	A	12461	112	7	HICIFYFFETESRSVAQAGVQWHDLSLQ PPPAFGK
12346	26247	A	12462	389	3	ALHEGAARGSPPPGGKKKKRGSPFFPMGN QAPQVPGKLGGGFGFWFFKSLPLQPGG KPGVFYKPKKVPTPKDPPPTLWGGWGT TGGPPGPLFFFFFFFETESRSVTQAGVQ WRHLGPLQPQPPAHAS
12347	26248	A	12463	26	349	CIMIDSTTGIFHCWWECEMAHPFWKAV WQFLFFFFFFKRGVYFFFPGGIKGPGFGLR EPLPPGIKGVPRPNPLGGGDLRPPPPPP INLGFPGKGVFMVWPGVGNFLI
12348	26249	A	12465	187	54	GYKNKPGQAQWLTPVIPALWEAKAGGSP EVRSSRPAPWPIWTRG
12349	26250	A	12466	199	55	I IQLRQQNSFLFCFDIESCSVAQAGVQ WHNLSLQLQLEVPGFKHAPSH
12350	26251	A	12467	107	3	FAHCLIGNSFFSFFFFFFFVGSCSVAQA GVQWSD
12351	26252	A	12468	120	1	GNWCRAQWLTLVIPALWEAEVGRSPEVG SSTRLGLPTRP
12352	26253	A	12469	105	2	YYLYFIFLFFLETGSCSVTQAGVQWKD LRSVTS
12353	26254	A	12470	238	405	FHICLFILKNQVSKMYHTVSCSLEI I YCCLLQWLTPVIPALWETKVGGSLEVRS
12354	26255	A	12471	425	1	LNPAPAIFFGGPKKNFFSPRGDKFFF FKRAPPPFFFFFFFQKKKKPFFPA QKKGRGFPGRALSQWPLAGFLKITQFPP WSRVFSPLLFFFDMESPSVAQAGVLW HDLHLPGSSDPPTPASRVAGITGVCHH A
12355	26256	A	12472	122	2	QNKYSELRMNTFGRPQWFTPVIPALWEA EAGGSPEVRSSR
12356	26257	A	12473	144	420	GAPRPISRPRGKTPGGGGKRGKPNKNGL GENPFPFKGKGNPPIFFPFLQNGPT PLVLGSANMGFYLYLKRKGPGKGREALR AEPGQFFY
12357	26258	A	12474	80	1	KGGQVQWLTPVIPAFWEAEAGGSPEV
12358	26259	A	12475	54	294	LIKSWQHRQEYVSLMSFIFPCHIWYQS QRSPGTTQIILEISDTGKNKYFNCTGSH RKHTHTHTHTHTHTHTHAHTTL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12359	26260	A	12476	364	234	EEEMGFHHVSDQDDLNLSWSACLGLPKCWDYRSETSRLASLPF
12360	26261	A	12477	288	450	PGTVAHACNPSTLGGPGWSRTPGLKRITICLGLPKCWDFRRELLPSLPCLLIIFL
12361	26262	A	12478	271	396	TISFLSFFFLFLFFFFFWRKSGRESRF SQKKKKYKKKNIIY
12362	26263	A	12479	289	2	GSCLLERKLTyrKDIHTKNPSVPHHHORPKVDKTPKTGKKQGRKTGNSKNQASPP PKECSSSPATEQKWMENDFAKLREKGFRRSNYSELQEEI
12363	26264	A	12480	323	1	YSMVYPYVFLTAKKDQLQVNNLTQLTCKSYQLYHCINHSTLQTHNISTLMILGHIPGLCIPVNLSEAWAATPALHFVKLLLTTELT HHVCRALDIIILAIVSLVALITS
12364	26265	A	12481	279	429	MNGQRKCVVYTYTLYTYTTEYYSTLKRKWPGMTMAHACKPNTLGGHGGWTA
12365	26266	A	12482	308	423	LTFKNTIGFFFFFTEFEFCFVPQAGA QGGDLSSLKAP
12366	26267	A	12483	272	474	MVSWGLSRAKIPWVLSFFFFFEKKSHFF FQGGGRGGDLSWEQPLPRSKGFSCFTLPSTRDYRPAGP
12367	26268	A	12484	84	229	LFKSVCHLLPLSSCSSHVRQACLPTFC HDCKCSEASPAMPLPVQPAEL
12368	26269	A	12485	392	3	TGKKKRFPFFPKKIFNSKPKQFSWRKKK LFKIFSPGGAPFPFGVQKKKTFFFYP FSPRTFFSIFFPKGPPKGGGLGPPFF POKRGGGFNSKWTWEKFPPLFFFFF ETESHVAQAGVQWHD
12369	26270	A	12486	76	1	KLISWTWWHMPVVPATWRAEAGDFS
12370	26271	A	12487	204	8	FFIFFFFFFFFFCKTGSHSVAAEQ EWHDHGSLQPPQSFHLSLPCATMPGL FFLFLFLT
12371	26272	A	12488	96	3	KKPLGQAMFFFFFFETESCSVAQAGVQWCDL
12372	26273	A	12489	126	1	KPPHPFLPFFFFFFETESHVAQAGVQWCVLGSQAPPPGFTP
12373	26274	A	12490	107	2	IAGRAWLMLAIPTLWEAEAGGSLEPRSSQPTCAT
12374	26275	A	12491	302	2	GGFGFPREKGGFFQTVLFGVPPGFFS PPVFKTGPVFFLGAQKKIFFFFPGGKIWFFLRGAPLFFFFFFFEMTSCSV AQAGLQWCDLGSQHP
12375	26276	A	12492	248	398	PTEQVTLGITAQSYSRVHINNRRVYDLAV GSGHPDGAIAKGSFVQRLKSY
12376	26277	A	12493	341	1	KTSHFREIYPLEHASSLSKKIETGALPC SQELLNSQENSVMNKFPCLNQLPQDVN SCIIRFQTKDTLKHTAIQPEAKTSLPC YTHTHTHTHTHNNHSIFELLCMQCDSYN
12377	26278	A	12494	95	3	PLFFFETKSCSVAGVQWQNLGSLQPPPP
12378	26279	A	12495	62	420	CAAKLCTEAHTAASADTHTSPhGSVSGLFCFHFPPhRRQRSRPGKPGAHRLAGRALSQKPVGSGATPHNLHQIRTQTNGLIQLLGDROAPWVTPVLPVLWEAEAGGSLEARSLRPA
12379	26280	A	12496	58	492	NSPPPPAPSQRTSPAAAASPTTGSSSA PCPASSWPRSSIALITFYDQPCGLSF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NNLAWKQNVLCFKERLLEKMFRRIQVLG LLVWTLIAGTEYFRVPAFGWVMFVAVFY WVLTVFFLIYYITMTYTRIPQVPWTTVC LCFKR
12380	26281	A	12497	2	198	RLQGILSAGFLVPGDTSVSSPRPRAAGS QSSTSRVLWKLSGAMRLRYVLVMGVSAF TLQPAHTG
12381	26282	A	12498	71	346	GMFMSTKETFTHYQPQNSDPAHTATAP GGLSAKAPAMTPLMLDTSSRKLVAWDGT TDGAAVGILAVAADQSTTLTFYKSGTF RYEDVLWP
12382	26283	A	12499	122	59	HQIYIYIHTHTHTHIYIYIYI
12383	26284	A	12500	220	3	PKKESVRCVAMKWIILLCLQTSLSHWSL PQSSLAATPCCLNLGTVDVLQGLGAVAH AWNPTLGGRDGWITS
12384	26285	A	12501	125	1	HVLVLSHFLEVLFLFFETESRSVTRPKR SSAVSAHRNIRLS
12385	26286	A	12502	373	476	ILTRDGVSLPRLECSGTISAHNLCCLL GSGDYP
12386	26287	A	12503	440	573	STWEDHLSLGNRGCEPRHLCTPTWVT E
12387	26288	A	12504	146	5	HPHLQTMNGAPIPQELTPLLKERDGLR CRGNRSPVPGIPRWSRDL
12388	26289	A	12505	140	44	AQGLTPVIPALWEDEVGRSPEVRSRSD WPTR
12389	26290	A	12506	247	420	LEISVTFSCSFGCLPKKHITHHTHTHTH THTHTHTHTHTYIRTIYTTLARPLSALH NF
12390	26291	A	12507	346	473	KAYIIGLNCFYETKSHVAQAGVQRDL NSLYS
12391	26292	A	12508	87	414	RTGVYRVGKDRSRSPDLLICPPLGLPK CWDYRREPPRPACPLLSHPSPPPHFSF LSPFLSFLPCSPFLYIFFPPPLPISL RWRLIPEGRFMAPLCLQMPGLGHT
12392	26293	A	12509	386	467	LLLFFEMESHISITRLECSGAILAHCNL
12393	26294	A	12510	344	472	KFLFPDPAVSLGLIYFKESKSFYQKDT TRMFIALFTIANTW
12394	26295	A	12511	424	132	RGEGPPRSGILSPVGPGETPPFLKKQK ITRGGGGPLFPPLKRVGENSFPPGGK SFHGAKFPFCPPPWATKRNSVSKKKKQ TKKGSRIILYNNE
12395	26296	A	12512	351	510	GGTDFCKQSKLQSLQPAVEIFIPGRVQW LTPVISALWEAEAGGSPEVRRSRPA
12396	26297	A	12513	362	463	NTITWLGAHAACNPHTLGGPGGRITWG QEFETS
12397	26298	A	12514	137	1	EEISLLLPRLECNGAITAHNHLHLPCSR NRRPGKAVHVRQAYSFQ
12398	26299	A	12515	251	592	GAFTGLAFTMAGGRPHLKRSFSIIPCFV FVESVLLGIVILLAYRLEFTDTFPVHTQ GFFCYDSTYAKPYGPEAASRVPPALVY ALVTAGPTLTILLGELARAFFPAPPLAG PV
12399	26300	A	12516	3	413	SWGGRKFLCPPRSLSGSRELHPAQGRDP GPLSSSGKRETGTHRETLGKKKVSSAPE AQQAGLRLSQALGGLCYDLSPLTEPRLP LAATAFPRPCPALPHQPQVPTMGVSSSL ISGHSFHSKHCRAQNKLRKSSHLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12400	26301	A	12517	115	2	KSHGGHGVVSVLVGLAMEVGLVLVWKEYDGAALA
12401	26302	A	12519	444	34	YCLRQKHTEYRRRSNLEMASSCLSGRKTCTFFTLTYQNLKMIKLSEEGTWQAEWLKS RPLAPNSKVVEAKEKFLKKIKSVTSLNT YILRKPNSLIADMENILVIHIEYQTSYN IPSSQRLIQSKALCLFNYLEMECRI
12402	26303	A	12520	1088	935	ILIIIFINRCEFLRSKKSSEETITQYIQSYKGFVDRTVMYNSNFFLKFLDYL
12403	26304	A	12521	2	347	AMAAGSRTSLLLAFALLCLPWLQEAGAVQTVPLSRLFDHAMLQAHRAHLAIDTYQEFETIYIPKDKYSFLHDSQTSFCFSDS IPTPSNMEETQQKSNLELLRISLLLIESWLE
12404	26305	A	12522	50	205	VVGESDRQSSGFWASSAHACNPTWEVETGGSLEARSWRLQCTMFASVKSTRP
12405	26306	A	12523	105	2	REVCSTIKVLRDLSSDRSNPGRFLSTNSSLYER
12406	26307	A	12524	279	455	RTKNWLALGGPPCFPGQYGETPSLLKNEKLAGHGGAPLYSRLRLRRGNLSLTPGDRGC
12407	26308	A	12526	305	454	LYFLFPFQIINRMVLFVFCFFETESHVSPQAGVQWRDLGSLQAPPPG
12408	26309	A	12527	363	459	CTILGQAWWLTVPVILALWEABAGRSPEVRGSR
12409	26310	A	12528	182	36	QHIVVFHKEHGQVRWLTVPVISALWKAEGRSPEVRSSNAAWHACRNSA
12410	26311	A	12529	388	530	KSFNFFPRDGLNCVPQAGLELGSSDP PASAFRVAGTTSVWHHSQI
12411	26312	A	12530	134	1	GHKKGVLFFFKTESRSVAQAGVQWCTLGSLQPPPLPAHATRPV
12412	26313	A	12531	230	1	KKFGFFPQAGPQGGHLHFTTLPAPWGQAI SQKREKPPFFFFFETEPHSVARLECSGTISPHCNLHLPSSNDSQASTS
12413	26314	A	12532	145	3	KKLEILSAIIPPKFRKEIFLFFFYETESCSVAQAGVQWRDLGSLQAP
12414	26315	A	12533	365	2	LEFFTSLIWQITLGFILNCPICPGVCIYIQFANTFRKFAFLFTNEIAYNIIILPLTKQDYTNLIKLIKHSFFSNFLKQLLFVFCFVFSLFAMESCSVAQARVQWRNLGT LQPPPPRFK
12415	26316	A	12534	313	475	FFWSCSSFQQGFGGGIIIIILRWILALSPRLERKWRDLGSLQSPSPGFKRFF
12416	26317	A	12535	124	3	MGSLIMGAELSVYRQVCDCKPQGVVCVCLCVCVCVCASTCM
12417	26318	A	12536	333	58	ACNPSKVRSCRPAWSNMVKSCLSKNAKITKEWWANFFVFVFLVEMMFHHVHGQLSLKLLTSSDLAASASQSYGITGVNHYAQPARTRGSR
12418	26319	A	12537	214	3	SDPRRACRCPEAPEQQRRPLPGGSVPALSIFFFFKTESCSVPLSPRLECSGVISAHCKLRLPGSCVPPAS
12419	26320	A	12538	146	1	MNLAFTNPPRPPQIILKPLLFILRRSHSVAQAGVQWCDLSSLLPPA
12420	26321	A	12539	195	1	IFIPPQAQKRGDPFLSFFFETRSPSPRLECSDAITAHCSLHLPGPGEPTTPPIPKSWDHSHVPP
12421	26322	A	12540	151	334	LLGLRLHKNHNLNPGGGGCSGTIMALCNI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLPRSSSSPTSASKVAGITGACHHACCLRYFLY
12422	26323	A	12541	314	402	NLNSGPAWMLPVPVIALWEAEAGGSPEVG
12423	26324	A	12542	339	3	GSCLLLEGKLPNRKDIHTENPSVHHHHQRPKVDKPTKMGKKQNRKTGNSKTQSVSPPKERSSSPATEQSWMENDFDELREGFRRSNYCELREDIQTKGKEVEIFEKNFERV
12424	26325	A	12543	31	365	RSVAMPTEDRATWKFNYFLKIIQLDDYPKCFIVGANDVGSQMQIRMSLRGKAVALKGNNTMMRKAIRGRLENNPALEKLLPHIRGNEGSVFTNEDLTEIRDMLLGKVV
12425	26326	A	12544	278	410	FSFKNVTAGRVWMLPVPVIALWEAEVGGSPVVKRSRTTLANMVK
12426	26327	A	12545	88	276	EVPQAHKRLPSAPQLRPLQAISTKGPCPPQSPQSPRPEGSSAHSRGEKRTREGRKEEKRKKK
12427	26328	A	12546	251	3	PVEDNSKRRFQTGEEKVTQEEQALTPWRTNFFCFSDRVSAQARVQCDSGSLQPQLPGSSDLPTSASQVAGTTGMRHHAC
12428	26329	A	12547	106	2	DEHLFPFLTSFETESCSVAQAGVQWRDLGSLQAPP
12429	26330	A	12548	225	1	GFFKKKEPHPRPCKKKTPPKLKPFWGGLNKKIPLSFVFSKKGPLPKKFFFFFFFFFFGSCSCHPAGVQWCDHGSLO
12430	26331	A	12549	218	3	VPPFGLVPGLPQIIPKGFPKTKGPPKGP PPGDKQKSGPPNKNFFFLRRESHSV AQAGVPWCDLGSLOP
12431	26332	A	12550	276	24	GPLKMVEAPPQNPLSPKNKIFFFFFFFETESHVAQAGVQWRNLRPLGSSDFPASDSRGAGITGARPHVQLIFVFLVKTGRKRR
12432	26333	A	12551	331	440	KSASSWSFNKSGWGWLTVPVIALWEAEVGGSLVR
12433	26334	A	12552	136	1	RHTGSKTTATALVDVFLLLFFETESHLSRLSCSGTTPGHCNLYE
12434	26335	A	12553	84	1	IFFCLFSFEMESHSAQTGVQWCDHGSLS
12435	26336	A	12554	3	349	HASGPEELSKDPSLVSQGQPHRKPGPKRCSSRPLGPPDKLGGEGKQGLLGFTLWLS GPIKPCDDEEKNNKKKKKKKKKKKLGG GPFKKKLFFPPGGGRNFFFLGAPKFFWAGRF
12436	26337	A	12555	257	417	KQLHLQGRFLSPSFLPSISKLFFFEME SRSVTQAGVQGC DLASLQAPP PGFT
12437	26338	A	12556	268	403	YMRLSFQDLVMPKDVAVDFSQEERWECLN SYQRNLYRDEVILENYSN
12438	26339	A	12557	286	426	DMLIKTCCHLVCEKKKKKKKKKKKKKKKKKKKKRGKALKKKPLPPP
12439	26340	A	12558	114	1	PLKEIANRHMKKCSSSLAIRQMOKTTM RYFTPTVMTA
12440	26341	A	12559	106	1	FFFFFFFFFFFFFFFFFFFEMESRSVAQAGVQWCDL
12441	26342	A	12560	118	2	KNYSNNLKTNAGRAQWLTPAIPALWEAE AGKSPEVRNW
12442	26343	A	12561	196	2	MCCFSKNWQEGAQMTPGFEPQDNSEKTKLSDTRLLFFFFERESRSVAQAGVQWRGLGSLQAPP
12443	26344	A	12562	128	3	RAPPPFFFEFETEFSLPRLECNGAISAHR



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NLRIPGSSDSPAS
12444	26345	A	12563	277	370	WSFTLVPPQGAQWCDLGSLOPALS RFKRFSR
12445	26346	A	12564	55	251	AMVIPTVPFNITINSKPLGHISFQLFADKFPKKTGENFHTLNNKDKGFGSCFHRIIPBFICQGDDE
12446	26347	A	12565	129	3	KYSVLRPGTVAHTCNPNTLGGRGGQITWGWEFETSLANVAK
12447	26348	A	12566	172	1	PPPKKKKPREPKKKNFFFFFGAISAHCNLCVPGSSDSPASPSRVAEITGSRCHAEPLY
12448	26349	A	12567	257	380	GICRPLLGGVLQSGATGVRDPLEEAVCP LAELKHCAGRSTA
12449	26350	A	12568	120	1	GVFLFCFVLFETESCSVARLECSGMISAHCNLRLLGSSNS
12450	26351	A	12569	250	2	IGKPKTPQFWFLKTKRGGPNAAFSFKKFFQLKPPPRVFLKIFSCQKKIFFFFFFETESRSVPQARVQWHDLSLOAPP PGF
12451	26352	A	12570	338	3	VSTPEKNFVFHTRGFSKSSSKYKVCNFF FQKKLGSPFSLKKVFPKPPYSCCSGRVSTAPYFLNPGPSTKILPFFFGPLGPEEKFLSFFFFFEMECSRVIQAGVQWCDLG
12452	26353	A	12571	5	556	ICCCLCFKINIFQLHFNKINFFCVTRSGPVTQAGVQWCNLSQOQPLSSKQS
12453	26354	A	12572	115	2	DRVSLVLVLAHCNLCRLGSSDSPASASRVAGITGARHD
12454	26355	A	12573	279	377	GQVQWLMPPVPAFWEDAEGLLQPSSSRPAWAT
12455	26356	A	12574	117	1	KTPLFFFFFFFEMESRSVAQAGVQWYDLGSLQAPPNGFT
12456	26357	A	12575	253	374	SLPGMVVHACNPSPGLGRGRRTWGRKF GTSLANMAKPCCL
12457	26358	A	12576	130	2	KFPGPFLLGFFFFFFFEMESRSFAQAEVQWRDLGPPQAPPPRFT
12458	26359	A	12577	132	3	RVPGPPLLFFFFFFFEMESRSFAQAEVQWRDLGPPQAPPPRFT
12459	26360	A	12578	3	370	LRKNCLNLGGRCESELRS HHCTPAWVTERDSVSKKKTLSVLMEKWPFPPLRPLALS RKKFPRGPFEQVTHLVKEVVSLTKPCCAEGADLDCYDERTSPLFAKSWERNFFFPVHPGPVEGCPK
12460	26361	A	12579	131	2	FIYFLFYFLFLETESLSVAQAGVQWHDVGSLQTTPPPRFTPTRA
12461	26362	A	12580	202	2	RMRKNQHKRAENSKNQNTSFPPKDHNSSQTREQWNMENEFDLTVGFRRWVITNSNLKEHVFSC
12462	26363	A	12581	109	2	KIFFFFFFFFETESRSVPQARVQWHDLSLQAPPPGF
12463	26364	A	12582	105	375	LIMILLPLQILVHSGTFCFLFFGFETEFHSTPRLECNGVMSAHCNLCPLVKTSPTASTQIS
12464	26365	A	12583	106	3	RPIFFFFFFQTESRTVARAGEQWCDLGS IQPPPP
12465	26366	A	12584	484	700	SSSWNRAF SRKKDKTWMHTPEALSKHFI PYNKFLGSTVEQPKGTEVVRDAVRKLFKARPIKSEGQKKK
12466	26367	A	12585	301	1	TQPKVRTQMKNNIFEHAFLSSTFPWPLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NLPADFYSATSQTKPDILQSMQKAFKNS GIGQAWWLIPAI PAALWKA EVGGLLEPR NLRPAWVYGKTL SLQK
12467	26368	A	12586	76	379	PLHPPASCPAPSL SCLIPGSPSDPLFSD SARPGWGRGWGRAPQLPPSPFFLYNLIK KWSRFCHQKKKKKKKKKKKKKKKKKKKK KGFFFWRAPPPFFFGGFFS
12468	26369	A	12587	109	376	LEFFKMSGVVP TAPEQPAGE MENQTKPP DPRPDAPPEYN SHFLPGPPGTAVPPPTG YPGGLPMGYSPQQPSTFPLYQPVGGIHP PVRYQ
12469	26370	A	12588	323	1	KKFCPPRFFPFLFGFQKKG TNPISPFSG GFKKNLGGFNPPRPWPSPQIGFFLGRS KELILGLFPTRIGIGGFFSFFFECETKS HPVMRLECSGVISAHCNLRLLVS
12470	26371	A	12589	262	1	GDPPTTSGPQTNPQKEHLMNFKSDSQLY EDTLAGRSVLINLTPQTLQPRWTGPYL VIYSTPTAVRLQDPPHWHRSRIKLCPS EKK
12471	26372	A	12590	284	374	TESRNWGWAWLTPVILPALWEAEAGGS PE
12472	26373	A	12591	297	387	GQAWWLTSVIPAFWEAKEGGSPDVRSSG LA
12473	26374	A	12592	206	407	VKPQNPRKAQKLKGLVYIHIYVYIYVYV YIYIYIYMYICRYISLTVVYTVNSKEKG LDTAAHTCNSR
12474	26375	A	12593	222	379	LTTGSI MGNFSLILVYTRKVMGSVQWL TAVIPLLWEAEAGGSLGSRSSRPA
12475	26376	A	12595	301	189	KKIQSQAQWLPPITIPALAEAGRSLEL KNSRSAWAS
12476	26377	A	12596	209	3	SVKPLFFINYQSQVVLFLFFRGR LKRS TISAHCNHLPGSRFSCGLPKCWDYRC APPTLKIDLT KD
12477	26378	A	12597	306	3	NGKKGFYMAPEPPFFHFFFFSPLFPTL FFFFIFLPLFCFALSFLVGSSSLSPRL CPMQHYFCDAWNTFDALIVVGSIVDIAI TEVNVSTWRLSLTVRV
12478	26379	A	12598	1	249	NTGAQCPLFESIQLQLFLGGGEDGVS LLLLRLLECNGAISAHCNLRFP GSGDPPA SASRVAGITGACRDHTCEPPRPVPPSS
12479	26380	A	12599	228	404	RLSSLSPVTEFGCLSPDLILKCDPWP TVTHTCNPSTLGGRGWITRGQEFKTSP VNM
12480	26381	A	12600	101	580	LSLTKNCALLGEETMMEQEMTRLHRRVS EVEAVLSQKEVELKASETQRSPLQDLA TYITECSSLKRSLEQARMEVSQEDDKAL QLLHDIREQSRKLQEI KEQEYQAQVEEM RLMMNQLEEDLVSARRSDLYESELRES RLAAEEFKRKATECQHKLLK
12481	26382	A	12601	464	3	CAIQQTLYEHPMKSSRLGPTQLKIFTCE YCNKVFKFKHSLQAHLRHTNEKPYKCP QCSYASAIKANLVHLRKHTGKEFACDY CSFTCLSKGHLKVHIERVHKKI KQHCRF CKKKYSDVKNLIKHIRDAHPQDMYCGR SRGSARMSRALPS
12482	26383	A	12602	140	1	WIGSFLSSEEDGTVVQKISGVQRSLSLY VYIHTHTHTHTHTHTHTV
12483	26384	A	12603	112	2	ESLRPGAVAHTHNPSTLGGRDGWINKDK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EFKMCERV
12484	26385	A	12604	139	1	KKRVKRGPPGGFKGLGGKFFSPKTFFF FFFETESCSVAQAGVQWR
12485	26386	A	12605	204	460	SGQNGEICHPRGFCTLPKAISLLIAR VCLKHFNKGVASLSQTANGCFEFGFSET ESRSVIQAGGQGGDPGSLQPPPPGSCLS L
12486	26387	A	12606	317	1	KRPLFKNIFQKPPFFKNGAPRKKGPRCIF GPNQKNPLFFPAPLSPFPWETKKGAGFF FWGFFPPTKIIGGQKVPFPPTFPFFFF FFETESLSVTSLECSGAISAH
12487	26388	A	12607	248	367	TQILSSGSGVQSSLHHPPICFIHTHTHTH THKHKHPHS
12488	26389	A	12608	2	387	QKQQRAGRETSTCSLRIISAPTMAFV ELSTKAKMPIVGLGTWKSPLGKVKEAVK VAIDAGYRHIDCAYVYQNEHEVGEATQE KIQEKAVKREDLFIVSKVQWCIWLAFNT IVPKSQWQSLQTPQRC
12489	26390	A	12609	258	23	MWERGIIRPQTQTLTGEPEGLDHGRSIS PNSVMNGIVPHISILTNLINGLNAPLKR PGIAEWIRIYQTSMMCCLQETGR
12490	26391	A	12610	176	433	DALSSAWGTVLGTQIPSHFTIILMLSP AWGSSSLTQTLFYVPSCAKRTGSYVLAR VGQKYKTLWLGAHAHACNPSSLGGRGRW IT
12491	26392	A	12611	312	410	AHMYRTCSRGVVSWLTPGIPALWEAEAG GSLEP
12492	26393	A	12612	3	289	VFEFLSRKLSYILRMFWTFKEFWLWLERF WLPPTIKWSDLEDHDLVFPVKPSHLYVT IPYAFLLLIIRRVFEKFPVASPLAKSFGI KETVRKVTPNT
12493	26394	A	12613	294	432	FMKLLLLLLLLFERRRSCFVAQSGMQGGYN ASLQPLPFGSSNFGSLPL
12494	26395	A	12614	138	375	SPNATCGHADPLPLCCLHICQALKRFT QTTTTFEGKPYLGILLYAVFFFLRLESCS VAQAGVQQPNLSSLETPPPSA
12495	26396	A	12615	232	1	GVPQRAKLRLAGLCPQAMDTFSTKSLAL QAQKKLLSKMASKAVVAVLVDDTSSEVL DELYRATREFTRSRKEAQKML
12496	26397	A	12616	236	419	LEMNGWVWFFPPVNPPTLWETEGVRDQP GQHEETLSLKIIFKISRHGMRGLGSQLL RRLRQ
12497	26398	A	12617	197	1	LCHSEGFLSRVSALLFTLLLLVLMESP PSVSPQGVQWPHFSSLQPLLPRFKQFCN TLP SGWDYK
12498	26399	A	12618	132	3	NSFMFHLFTYFEMESCSVAQAGVQWRDP GPLQAPPERVGGRV
12499	26400	A	12619	255	2	MNSLNSFTDIAVIPLHYNRILPHFKIIL SYFLKSKFQVKGIGRVKWLTPVIPTLWE AEVGRSLEPRNCPAHQPGQYKGKILYKK
12500	26401	A	12620	141	2	FHFTYIIITSCVCVCVTSRFRVARLECSG AISAHCKNHRPGSSNSPA
12501	26402	A	12621	274	421	TYVMEVCCTYYFLAQVLSLAPFNYFIIR PDPRTDPRDPDPDPDPPEPRP
12502	26403	A	12622	132	2	NQSIKKKIELQGFQSRSGRGKGVQWL T HIIPARWEAKVGRSP
12503	26404	A	12623	390	86	LFPPFYQNTNGMAPGNQIPQGFSSRFFF FLRQVLALWPSLEYTGETDQCRLKCSS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLSLCSSWDNRCAHPPLVNILFYVETGS HYVVHIGLKLHHSRYPG
12504	26405	A	12624	297	396	IIRVRGRAQWLTPVIPALWEAKAGGSPG VRKSR
12505	26406	A	12625	303	381	KFHLVPSINTMSGSQELQWMVQPHFL
12506	26407	A	12626	318	152	GDKRRLVSKKKKNLWNFGRIQWVPPVIP ILLEGEGAGGSPEVRSFRPTGQQSMTPF
12507	26408	A	12627	48	388	QLGNGKVRLLYQRHSSSFFFFWGGFPP GPQGGGGPNLGPRESPPPGVKGTPPPS LLEGGEPPGPPPPGNFWGFWKKGLPL YPGGPPTSGPKGEAPPTPKGGGGIKGL P
12508	26409	A	12628	116	3	KVATNQAWLMPVIPALWEAKAGGSSEV RSSRTADAW
12509	26410	A	12629	227	400	VLFVLFCKEWHVFIFLILPVYSYKKKK KKKKKKKKKKKKKKKKKDSQKKD
12510	26411	A	12630	182	3	TNWLFPFPKFGPVPLFPLPFFFFFET GSHTVAQAGVCSGAILAHCNLRPLGSSN TPA
12511	26412	A	12631	134	473	ASTIMDLLFGRRTPKELLRQNRALNR AMRELDRERLKLETQEKKIADIKMAK QGQMDAVRIMAKDLVRTRYVRKFVLMR ANIQAVSLKIQTLSNNSMAQAMKGVTK A
12512	26413	A	12632	100	462	QLLLCCCCRQWTA FNVPASPAPPPAWA HMAPSLLEPPSLLVTOICKLSAFSGPSI NAFLLSKKKKKKKKKKKKDRGGAPLKK KK
12513	26414	A	12633	313	441	CWELLKWLVCFLCHIIKTNNCWAQWLTP VIPTLWEAEVGGSL
12514	26415	A	12634	129	400	VSQQCWPTPPALYSISRQALAAS PQGRP WDLQPTMPESP LLPRAPAWPKLRRAL PPAPRCLGPSTAQGLRSAGAWCGTGRHL HLRPQC
12515	26416	A	12635	308	399	EIRGWTQWHVPVIPALWEAEAGGLPEVG SS
12516	26417	A	12636	285	390	IFGVLINSFIYFETESRSVVRAGVQWRD LGSLQPP
12517	26418	A	12637	260	2	GQGPFFFGGRGSPKKKPKLKGFFLVGGS KTQFFFPKP KGPFGVFFFFFSQTASRS VTRLECSGMILAHCNLRPLGSSDSPASA SR
12518	26419	A	12638	76	3	ALQVQWLMPVIPALWEAKAGGSLE
12519	26420	A	12639	219	484	LGLQEPDLDEKPILELPLAELAQQLQTE ELSLESILCSYLKQALKVHQEVNCLMIF LGECEEBLLALKKLKKSERGLLYGVPM LKDT
12520	26421	A	12640	33	462	EGLSWG YREHNGPIHWKEFFPIADSDQ SPIEIKTKEVKYDSSLRLPSIKYDPSSA KIISNGHSFNVD FDDTENKSVLRGGPI TGSYRLRQVHLHWGSADHDGSHIVNGV SYAAELHVHWNDSKYPSFVEAAHEPDG LAG
12521	26422	A	12641	2	414	SGPAAPATPMSIFPELYFNVDNGYLEGL VRGLKAGVLIQADYLNLEQGETLEDLKL HLQSTDYGNFLANEASPLTVSVIDDRK EKMAVEFRHMRNHAYQPLASFLDFITYS YMIDNVILLITGTLHQRSIAELVPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12522	26423	A	12642	161	463	KEKARGRPKPLLLLPITSATTAMGLTIS SLFSRLFGKKQMRILMAGLDAAGKTIL YKLKLGEIVTTIPTIVFNVETVEYNNIC FTVWDDGGQERIRPLWN
12523	26424	A	12643	124	2	TVFGGQAQWLMPITIPALWEAEAGRSPEV TSLRPAPWRTRG
12524	26425	A	12644	258	454	NRPELCDYQGLREDSKRKGEINQTACQF LWPRQKMSSQTKFKKDKELIAEYEAQIK EIRTQLVEQ
12525	26426	A	12645	636	182	APLERPSMIPPRCSGGQPSDLRSSPAQG TERPALGDRKGTPIAEFGGAGRAEAPP PRGSRQRFQRRQTNAHTKRVTRLASA APARHSPAFTACRQVGRPLRSARRSGKK PHLTVWCPSFQDPIQDTTLQIILSL GGDTFSDFPCS
12526	26427	A	12646	199	414	IYHTSRSLDRKLRAQRYDELPHYGGMD GVGVPAAMYGDPAHPGPIPPVHHLNAGP PFHAKQNYGAHAPHNP
12527	26428	A	12647	130	3	DRGFLCVHTPLKKKKNTHTHTHTHTH TNHTHSHHTHTTK
12528	26429	A	12648	192	443	LLLCWAQESLGTLGENTASSHTAGLEWE SPLFACWFFWGFCLFVWLFVWFEPKSGS VLTLECSSVITAHCSLDLPGRDPPASA
12529	26430	A	12649	393	179	LHSRVQRSGCFSCVSNVPTGGMHFTRS SPQSNQEADQARWLTPVILALWEAKAG GLPELKSSRPAAWATP
12530	26431	A	12650	263	2	KAPLLVYKWEPNPGGGNFSPGMGTPNTF GVRFGGETKELFFFFFTGSHSVIQAGV QLCNLDSLQPPPPSVKPSQYSWDHRKQS NTK
12531	26432	A	12651	355	111	QDFCFIRLHPLSLFSLVFLECTKISLLD WRMLFPLLDGPPHLALSSLVSPINTWNY SFQQLMMFRDVAVDFSQEEWECDDL
12532	26433	A	12652	271	3	RQLKNILIFFSHKNMLSIKHIIYNYTLF LKSAFI FNLETDHLNCFPGSISAKSYFI LFYFFETEPHSAQAGVQWRDLSTLQPP PERFT
12533	26434	A	12653	333	2	PPSPGVFGNPPSPGDPGLKTFPPRGP PRFWGGGFFILAPFPFGGLFPFPLPP SQGPPFPFPFPFPFPFEMESRSVSQAGV QWRDLSSLQPPRARFSDSPLYFLEGR
12534	26435	A	12654	310	444	TYLSNIFYFILFLVETESPSVAQDGVRW CGLGSLGPPPPGFGFRFS
12535	26436	A	12655	336	411	DQPGQHGETPSLLKIQKLVECGGAH
12536	26437	A	12656	114	2	GIFFFFGLESRSVAQAGVQLCDLNSLQ SPPPGFKQF
12537	26438	A	12657	191	1	KNFILTFSFRGAKNGDVFFPPPGYIQTG ENFFFFFLKWSFTLVAQAGVQWNLSS LQPPPPR
12538	26439	A	12658	1	445	LRTGSEFSGRDSKGLAAEPTANFGLLL ASIEDQGAGGGGYCGSRDQVRRCLRANL LVLLTEAAGVAGVALGLVSEAGGALAL GPERLSAFFFPGELELLRLLRMIILPLVG CSLIGGANSLDPGALGRLGAWALLFFLG TLLASAL
12539	26440	A	12659	2	224	ESTASRIAFEAWQPETLPKGLNYSGASP VVLNAVLPKKKKKKKKKKKKKKKKKKK KKKGGGVFKKKKIKGGGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12540	26441	A	12660	96	1	GLKDGGRGQVQWLTPVISAPWEAKVGGSP EVMS
12541	26442	A	12661	1	457	CWVHLQKGCHFTLGRHLHSGQAEALLTSQ TGRPGRGAPHIPDGAARQRRSSHPRRGG QAEALLTSQTGQPGRGAPHLPDGAAGQR RSSPFRRAAGQRGSSPFRWAAGQRLS SLPRQGGRAEALLTFQTGRPGRGAPHIP DEAAGQGGAG
12542	26443	A	12662	175	351	KGIFFFPSPWKAGGAIWFKGTFAPRGKG NPPPNPSGEGGPKKKKPGPQIPRGPPLG PPV
12543	26444	A	12663	247	401	SSNQEPGCKGPCVLTNFYFILGRAWWLM PVIPAIWEAGTGGSPVRSWRPT
12544	26445	A	12664	152	251	RENSCCFIKKKKKKKKKKKKKKKKKKKK KRGAP
12545	26446	A	12665	2	365	APTFRSRLRHASCTACRTVSTDTSSLRR ADPKGRSALLADIQQGTRLRKVTQINDR SAPQIESKGTNKEGGGSANTRGASTPP TLGDLFAGGFVLRPASQRDVAGKEEFI LAPLWTVSP
12546	26447	A	12666	179	1	LELSKSGSHWMRHFLRSFYSLISPQLN TTVWPTTITPILLTLFLITQLKILNTNY HLP
12547	26448	A	12667	279	35	NQAPFKARFFTTFKNVFLKEIKKKRCWS GAPPIIPPPWGGGGGGPPWGGNLSPPGP PVSTPFNGAQKKKKKDRYGGACL
12548	26449	A	12668	299	399	ISIKKQRKGPVQWLMFPVIALWEAKAVG SPEVR
12549	26450	A	12669	1	385	KMQNRGFFFLTFLALLGLTSGAAKKKNK GKKAGPGSKSPNWPWGPCPPSSKDCGGV FRKGTWGAQTHGIRGRPCNWKKEFEAN CKSKFKNWGAGDGGPGTKVRQGTLLKAP SIKQGETIRVTKPCT
12550	26451	A	12670	357	1	AGKIAKICPVSSMQAPTGGFPVGGNDNQ GQAPDGGQFPPLQQNTSSPDFSNENSP ATPPEQGGQDAPPQLEDEEPAFPHTDL AKLDDMINRPRWVVPVLPKGELEVLLKK GIDFSKK
12551	26452	A	12671	107	373	TGNYTPLEDCAEQMRLIAQVHLLSTRV KQQQVKIKQLLQNEVQFLDKGDENTVV DLGSKRQYADCSETFNDGYKLRGFKIK PLLNP
12552	26453	A	12672	196	45	YLYFHGSREKRLAKKYDKLFKECCIAD LSKYKENKVCFFPHIYGKRFLLFK
12553	26454	A	12673	33	448	KEGAERAGAAAPVWSFLDRRDSARTRS GTSLSADMGMKTPDFDDLLAAFDIPD IDANEAIHSGPEENDVPGGPGKQPQCVG SESEHTASASAGDGPVPAHASDHGLPP PDISVLSVIVKNTGLSRAGWRPWVDV
12554	26455	A	12674	250	29	KKQTNMWQSPYEDYRIFYTTISSLYHLS IYPPIYLSIYLSIYLSIYLPHTLSIITD YVSILEHELRLPLWRIQP
12555	26456	A	12675	377	442	SDRQWWCMPVVPATWEAEAGES
12556	26457	A	12676	1	553	RIFPGRFRVVKLPSCPDPAWGTRLLFWV AFCLLGADHTGAGVSQSPSNKVTEKGD VELRCDPISGHTALYWRQSLGQGLEFL IYFQGNAPDKSGLPSDRFSAERTGGSV STLTIQRTQQEDSAVYLCASSLATAWHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RLLPAAHKPHPSLSLQLLDTLNRGFSLLL PHGKQVDLDLSLSFG
12557	26458	A	12677	232	3	GWSSDCQQRARVIEEKHSRQKGHIAENP SVHRHHQRPKVDKTTKMGKKQNRKTGNS KTQSASPPPKERSSSPATCI
12558	26459	A	12678	134	3	IFIVEFGGKPFSCSTISLSQWLWCLFTG IGELLWGQVSTGTLY
12559	26460	A	12679	212	47	NGTHPHGYTLHTHKHTHSCAHTHTHTHS LLLVRSFLLPQKNTTISFRSCCKLGKP
12560	26461	A	12680	224	2	MKMASFLAFLLLNFRVCLLLQLLMPHS AQFSVLGSPGPILAMVGEDADLPCHLFP PMSAETMELKWVSSSQCI
12561	26462	A	12681	35	397	KPLISONKIHVSVSSSQTFGFFFFFFFFGE KKPPFAPRGGGKGGPPPLPPGGGNRAP RGEKKGKGGKPPKPNPGAFPPQKEKTPG GGGGKKKTPAPPTPKEVDQPLPRREQRG PGRLLPRGA
12562	26463	A	12682	188	514	HTTHLVYVLSMAAFFFFFFFFFEKNFLFAPR VEKRGKDLGSLKLPPLPGFRHFSGLTLQG SGNNGAPPPSPVIFLVFFEKRGFPLVGR EGLILPPLQAPFCISFRGAINGPS
12563	26464	A	12683	366	3	ISQTQTQWTDWVSLELQGCCLAHRTVA IPQTRSFPPPLMISCMTLFSLQLQMDRAF PFPPTPTPTIQQISTSPATWPLTHLH STPGLSVEYSSNTHKSSLSPTSQWIRVD PMLASPTV
12564	26465	A	12684	99	1	SSCIRFFLEQAYGQQSYGTYGQPTDVSY TQACI
12565	26466	A	12685	247	31	FLKEKRNQFYLFIFQRWLDPNKPIRKQL KRGSPYSLNFRVKFFVSDPTKLQEEYTR WVYGYIFLENIVKTLI
12566	26467	A	12686	416	253	PSPMTIPVTGAPRDADLWSSSHAKMLAQP LKSDSDVEVRLGSSQIFLCWRPSFNL
12567	26468	A	12687	116	3	CLLGRMWWLMPVIPALWEAKAGRSLEVR SLRPARPMY
12568	26469	A	12688	380	1	SPSSKLGLWSKHVSPLLCIGVCPPPVVS MAELRQVPGGRETPOGELRPEVVEDEV RSPVAEEPGGGSSSSSEAKLSPREEDL DPRIQEELEHLNQASEEINQVELQLDEA RTTYRRILQESASV
12569	26470	A	12689	157	488	REFVSQGGSHLKAQVRLEALLLTIGTPP WAHLSILHMTAMGQRENKREAASSRIQV LLNHSQAIKQESIILFFEMESGVWPRLQ YSRMISASCTLFLSGSNNSPVSAPRI
12570	26471	A	12690	514	3	PSIRAGLLCGSAENATPFLCGITMAAGP LYTYPENWRAFKALIAAQYSGAQVRVLS APPHFHFGQTNRTPEFLRKFPAKVPAF EGDDGFCVFESIAIAYVVSNEGLRGSTP EAAAQVVQVVSADSDIVPPASTWVFST LGIMRHNKQATENAKEECMRPLRVSSSLV GP
12571	26472	A	12691	304	4	AESLRVAHERLDTRSTSSDIFNFPQTQS NLEMNSEILESANYQSSTSYSINTELS LFSKVNKGKSTEFQRMKTLQVKDQAITT RVQVRNLVYTVKINPL
12572	26473	A	12692	221	2	VGPATRDLCFADEPVGGRQKQKQWVWL CLSPNRGLAGRPDTLHITCASAHMRHTT CMHTRHAHAHVHTHCI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12573	26474	A	12693	3	205	YMLCSILSTQEAFTICLGEKFTIYLFYTL FRDGVSLLLPRLECNGVILAHCNLRLGD RARLHLSKKQK
12574	26475	A	12694	233	3	IMGPAHLFKGNHNGGWLMYKAFFFLF FFKTGSHSVAQAGTIPVHCNLRPGSSD SPAPASRVAGNTNVPHTTLY
12575	26476	A	12695	408	3	PAREMEKFRVCVRKRPLGMREVRRGEIN IITVEDKETLLVHEKKEAVDLTQYILQH VFYFDEVFGEACTNQDVYMKTTHTPLIQH IFNNGNATCFAYGQTGAGTYTMITGHE NPGLYALAAKDI FRQLEVSQPV
12576	26477	A	12696	123	631	REAVQCGKSGCGGFGSRDSRSSGAVSAA VGDMGDPGSEIIESVPPAGPEASESTTD ENEDDIQFVSEGPSRPVLEYIDLVCGDD ENPSAYYSDILFPKMPKROGDFLHFLNV KKVKTDTENNEVSKNHCRLSKAKEPHFE YIEQPIIEEKPSLSKKETDNLGASDCW D
12577	26478	A	12697	429	629	LALLYPLKWVGKPVNFMEEDILGPLPPP LNEEEEEAESEEEEEEEENPVHKIPDS HEITLKHGTKT
12578	26479	A	12698	158	404	LPLLSVERLVEIYAYTFIQDLFSASNIP YSSSVFRIEMDQPRTHSGPTTASNPA STNSSAPSATNSKQERSSSSLSKPS
12579	26480	A	12699	185	3	HRRPTISIPSSVIHPAMVRLGLQYSQGLV SGSNARCIALLRALQQVCPILLSLMTQP HLVY
12580	26481	A	12701	181	3	TVWASMFLSAALRARAAGLAHWGTHVR HLHKPDMQNGAGGALFVHRDPRENNRDT PCI
12581	26482	A	12702	373	1	ILVQERDSQVRVIRMIDKLVSSRDVRGRG VEKQMTDHRVIYSVRKLQKRITPEPFIP SRTTPKLLFLLVLP SGKTPGHPVSSRTI PEPPLPTEPLERIEHPVP SGTIPKPPE PPLPIEPHETMY
12582	26483	A	12703	272	508	TKLGKKQNRKTGNSKQQSASPPPKERSS SPATEQSWMENDFDELREEGFRRSNYSE LREDIQTGKEVENCEDNLEE
12583	26484	A	12704	341	1	VPQHPRPLAPPSLGPQSWPLMEGSRPR SSLSLASSASTISSLSLSPKKPTRAVN KIHAFGKRGNALRRDPNLPVHIRGWLHK QDSSGLRLWKRRWVLSGHCLFYYKDSH V
12584	26485	A	12705	187	365	WEPSCRGPSAFKPTRCQSYDWACMCGAE GRSAMEQPQEESEPEVREEEIEEMAHAE GTP
12585	26486	A	12707	238	596	LWLVRVKYSIMSGAALGLEIVFVFFLAL FLLHRYGDFKKQHLRLVIGTLLAWYLCF LIVFILPLDVSTTIYNRCKHAAANSSPP ENSNITGLYATANPVPSQHPCFKPWSYI PDGIMPI
12586	26487	A	12709	131	2	DRVSLSPRLCSCGTILAQPSRLKQSSHL SLTGSWDYTHAAPCI
12587	26488	A	12710	151	2	YRQGLILLPRLECRVMIMALCNFESPGL SDPLTSASRVASTTATCHHTC
12588	26489	A	12711	151	1	NFPEFDHFTVGCLRAGSSLIHYWWECKL VQSLWKAVWRFIKDLKIDLPLY
12589	26490	A	12712	28	411	RVVPPARPAGEPREPHVSWVMKLNPPQAP



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						LYGDCVVTVLLAEEDKAEDDVVVVYLVLFGSTLRHCTSTRKVSSDTLETIAPGHGCCETMKVQLCAFKEGLPVFVTEKYFLLPRMYRYRCLYTYPSSAAV
12590	26491	A	12713	351	675	ENPRHTFIYSLPLGLQKHQVLTVDIGFGTAIMTVGKSSKMLQHDYRKRWILQDGRIFIGTFKAFDKHMNLILCDCDEFKRIKPKNAKQPEREEKRVLGLVLLRGEN
12591	26492	A	12714	326	457	ACSHHQKRSQAPPPAHLWPDPCPHGSLPLLNPSCVNCNPGREVSPT
12592	26493	A	12715	200	1	TITKVCVFTRTCGLKGLMAKALFDQRKDRESETECQVWMLTPVIPALSEAEGGLLEPRSSRPV
12593	26494	A	12716	208	405	KKERENKKHTNKKGRKKMVHICQWHSSLHRKFQGIYRKTGTGTGWAQWLTPVIPALWAEVGGPPEV
12594	26495	A	12717	157	3	AKETPTHKGSCKKKFFFFFETESRSVAQAGVQWRGLGSLQAPPPGFTPCI
12595	26496	A	12718	1	472	SPAILPRLAILPYLLFDWSGTGRADAHS LWYNFTI IHLPRHGQWCEVQSQVDQKNFLSYDCGSDKVL SMGHLEEQLYATDAWGKQLEMLREVGQRLRLLELADTELEDFTPSGPLTLQVRMSCECEADGYIRGSWQFSFDGRKFLFLFDSNNRKWTVV
12596	26497	A	12719	537	1	LHTMNGGNESSGADRAGGPVATSVPIGWORCVREGAVLYISPSTELSSLEQTRSYLLSDGTCKCGLECPNLVFPVFNFDPLAPVTPGGAGVGPAEEDMTKLCNHRKAVAMATLYRSMETTCSHSSPGEGASPMFHTVSPGPPSARPPCRVPTTPLNGGPGSLPPEPPSVSQACI
12597	26498	A	12720	369	3	AAKIIPATRKASLELELPSSPDSTGGTPKATISDTNDALQKNSNPYITPNRYGHQNGASYAWHFEARKSQILKCMCEGSSHD TLQELTAHMMVTGHFIKVTNSAMKKGKPIVETPVPV
12598	26499	A	12721	230	3	KFFWVLAGLTGKNSDASASLNQVHISPLLFSRHHFSLGLPLSSPVLLQGSKRRLATLRALESASLSQHPHPV
12599	26500	A	12722	26	110	REQYAEGNMRGPAPGKKTSGLQQKNVEV
12600	26501	A	12723	224	1	WQNDQASDPPKYSFTSQCLSFLARLARYGDVVFQIRLGSCPIVVLNGERAILQAMVQQGSAFADRPAPAFASFRV
12601	26502	A	12724	120	530	KKVARGSRSRERSRRRRSRPKAIT\NRT*GTRCTPRRWRSTVLGMRSCTRAR*QRSGLSRGHTRSAGLCDHGSVRAGSGDGDGTGGGDRRLGLGRDSLILLSSSSQSAAFSSASGSSSFFSATQPLRMLLEYFWL
12602	26503	A	12725	434	222	KEEKSREGEVKEQD*EKDREEEVEKSRE/RRRRRRRRRRSEV*YRKGRRRREREDILVAERSHRSFRNSIPSTL
12603	26504	A	12726	268	370	SNILIHMSMFFFFGTIPSV*KNLBA*KTGPDGDFIDKLYITFRGELTTFPHILLH*FTEGAVLFNSFSK\AASITLTPKPNYDIMRKENYSPISSYIWNQCSFFLEQIFPLSFKLNCPLIIPH
12604	26505	A	12727	103	636	VCFISMKQPHGSRHPPCS/PPRPGS*VCQQSRPLGPQPSAFGQLA*HRRGLLGLQG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PRSPMQPVPHGGRVSGQTLPGKPTPKRP PGPAPRHGGHSLWK*LVCAQPPPRP*S *ASQAVFTLQVPGKPQVWTPCPVPVRAP TP\PLSNGGLGVSERH*DGH*QAPTSP* PRCQGAGGEGPQ
12605	26506	A	12728	1193	1638	GLGFAMLPRLALNSWPQGDPSVPASRAA GTRGVHRHTQLQVSFNYYKVLAMHSGSQ L*SQHFRKPRRSDHLRSGVRDQSGQHGE TPSL/LKNTRISWAWHTPLVPATREAE ARELPE\PGROKIASERPVKPICTASLG NTCETPPQKK
12606	26507	A	12729	304	101	RHLHWPCPSPLAPTDPDISHCPEPPKSQT SP/CPGT*CLGFLKCPSSCHFA*K/PLH PSEPARKSLAPDTCF
12607	26508	A	12730	91	264	SQRSISGLRVKENLIFVMIMFPPIYSSQ TFWSQTFMLKIVFMGISISICYIL/NT EKNLGGQWWLAPIIPALWEAEAGGL*L RVKENLIFVMIMFPPIYSSQTFWSQTF MLKIVFMGISISICYILKLRKI
12608	26509	A	12731	1026	406	LAHFRSQIFSFSHILVHFERMVLNRYRY LACVRRVVRFLHVLAYFGRIVLKRYRYF LVHFRREVFRRHMLACFRMVLICYFL VLRKILLIYVTFITYFRKVFLRHNFLRG GY*RKYFGYAPRWLSFFLYRCQCFHLYF LFYLVLRHLQF/CCFVVSFCLFDFLFL FSAACVFSVLQIAIVMFPFHALQLFFF* VVLCSNSRFQ
12609	26510	A	12732	1508	157	QDVGGSGFKVDTHPRGRMASIFSLLTG RNASLLFATMGTSVLTGTYLLNRQKVC EVREQPRLEFPSSADYDLRKHNNCMAEC LTPAIYAKLRNKVTPNGYTLDDQCIQTGV DNPQHPFIKTVGMVAGDEESYEVFADLF DPVIKLRHNGY*PQG*LKHTTDLASKI T\QQQFDEHYVLSSRVRTGRSIRGLSLP PACTRAERREVENVAITALEGFKGDL\A GRY\YK\LSEMTEQDQORLIDDHFLF\D KPVSPLLTCAGMARDWP\DARGI\WHNY DKT\FLIWINED\HTRVISMEKGG\NM KRVLRS\FCRG\LKEVERLI\QERGWE F\MWK*AP*EYILT\CPSNLGT\GLRA\ GVHVRDPQSFSQDPTAFLKILEKPRTPR KRGHKVVDIAA\VADVD\ISNIDRIG RSEGEL\VOIVIDGVNYLVDCEKKLERG QDIK\VPPPLPQFGKK
12610	26511	A	12733	261	487	TGSETDCAKQASFLPREVPTVAEMKME LLKNKQFW\RGVVAHACNPSTLGGQGGW IT*GQEFETSLANMAKPHLY
12611	26512	A	12734	382	668	YKRITDIFVDSETVHILINKRQSCRIPG FIQLVQLISHQLAAPRDYTVSHSVAQAG VQW/RNLGSLEPLPPGFKRFLCLS*HAL KNLSSCDTPPQY
12612	26513	A	12735	401	27	GDRAEESAEPRAWSHSDNSHRYTTLFIC LTHTHVHNPVHS\HTHTHTHTHTHTH TVSHRHTETPPLLLKQTGLKFY*NSRDD TPRSRPGSSGLQRLSSPPVPFPQGTVE ASADFCGHDLLT
12613	26514	A	12736	202	182	KYLPFIINLITMNLFFETHSCSVGQA EVH*S*LKPMPPG\SSDSPASAFQVSGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TGSPSSSWLIL*FFLKIGFTKKG
12614	26515	A	12738	319	2	QNTPPHIYIYIIPRVDAFLFLFLEMSYSVY VVAVLSPLYFVNKLALTLHCRLALNSFL HKIQEPS\LGSGSG\PLSCNTII*RLCL RSLHLVFRSLWILPICDSSSVF
12615	26516	A	12739	1363	2000	DRVFVIPGWKCSGTIKVHCSLDLPGSSN PSTSAP*VAC\ATGTYPPCPGLNFLYF* MEERGFTQVA\QAGSQNSWGSKPNGTSE ASPKVLGMNKP*NLPNPGRSILN*DGSI RYKDNYP/WEPPKRSYKCLRQKKS I*L SAGPRDYEASQPRKNYPISLLTFTCTSS LHFNPTELTCSSQLQKSIRRLKSEESC PPLPACSLKHTQAIKIF*RLHRTA/L FYLLK*NCFRN*S**KYFLSVSNLKI/ QWVRSSLHPGAPGYTPTV*RPKHKS NVL I*IQS/ITRCLFYILVYMRITIFPLQLFL SKHPSTYKEDFA*VLPLSFFFFEMESRS AARRSLSSLQPLPRLKRFSRLSLLSSW DYRCAPPGLASPSILSS*GSCCSIQFIL RMSTISHAINVLVLKNTYLVLSASEHS LKKPC
12616	26517	A	12740	1696	743	GGQIMRSGVHDQPDQHGTEL SLLKIQKS AGPGGMHL*SQLRLRLRQENRL\NRGCS EPR/SRHCTPAWATEQDSVSKKIKK*KK *NHLESKQQQPALEPPEQAGGQLRKTE QLQDGRRELAADMTL*PGHSKRLGALPR PLLSAYYFNKVHAARRQAYLETPTGTFTS YQREEGEQALILGVEAQASSPTVFHRER RQSQALCSHRKSQEAPVRPAHPPRRVPG LGKPSSQGLSAHLGQDRAPAPRRASWDQ RSQAPISVTFPSPVLDKESVPCGPGFPG HAPAPRGIHGATWEGAHSRGYPGHFLAL PQHNSDEQRPN
12617	26518	A	12742	2473	445	RGARRRRRRSRHRRRRHQSRPVRAAPRQ PEQRRRGAPTHGPQLIMMDLELPPGGL PSQQDMDLIDILWRQDIDLGVSREVDF SQRKEYELEKQKLEKERQEQLQKEQE KAFFAQLQLDEETGEFLPIQPAHQHISE TSGSANYSQVAHIPKSDALYFDDCMQLL AQTFPF\VDDNEVSSATFQSLVPWYSPG HIESPVFIA\TNQA\QSPETSVAQVAPV DLDMQQDIEQVWEEELLSIPELQCLNIE \NDKLVTETMVPSPEAKLTEVDNYHF\Y SSIPSMEKEVGNC\PHFLNAFEDSFSK HPLHKNDPNQLTVNSLNSRM/PTVNTDF G*WNFILVF\MAEPSIRQAWPSPATLS HSL\ELLNGAHGCFDLFTL/CKAFNQ NHPEGTA\EFHGF\DSGISLNTSP\SA SP\EHS\VESSSYGDTLLGLSDSEVEEL DSAPG\SVKQNGS*NTMYSSSGDM\VQP LSPSQAEHFTCMDAQCEHTRGKDLPV \SPG\HRKNPISQDKHSSPLGGLISQR DEL\RAKAL\HIPIPCRKKSFNLPVG/D FNEMMSKEQFNEAQL\ALIR\DIRREGV RNKS/AAASGICRKKENWENIVELEQDL DHLKDEK\EKLLK\EKGENDKSLH\LLK KQLSTLYL\EVFQHAYRDEGKPYSPSE YSLQOTRDCGNVFLVPKSKKPDVKKN

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12618	26519	A	12743	6	457	RPRNRPGIRVDPRVGRVGHAPHEGLVP ERMYRGSPTACETQAAA*ERAFGPSST C\RLPIPRMSTSVPPQGHWTQRVKKDDE EEDPLDQLISRSGCAASHFAVQECMAQH QDWRQCQPQVQAFKDCMSEQQARRQEEL QRRQEQAGAH
12619	26520	A	12745	297	12	QERPVRMLVLHFGRLRLADHLKLGVRDQ PGQYGETPSLLKIPKLSGM\MWAP*IC
12620	26521	A	12746	98	428	YNTSFNETVLLLTPTITIDCLYTRKDAI APESACGVCPSSLGVGA*IPKVVIRLD LSKKHVTAYGGFMCAKCVLDRINRAFL IDEH\KIVPKV*KALSQSSKAFCEHET
12621	26522	A	12747	3	638	LWLWSLCVWVAVSLPLQFILGSLHPCQG QASWREVDLLHEGSQEASSKPSSGSVPV GLLLDQEMVTPLLVCICGILLHQEMVSP LLVYTRGILLHQEMVTPHPGLYPWDSPP LDGHSPPGLF\RGAAAPS*GG/PLPVLV YTRGAAPSGDS\PPPPGLYPWDT\PPS GDRHSPPGLYPWDTPPSGDGHSPPALYP WDSPPSGDSHSPPGLFPRG
12622	26523	A	12748	2	333	DMVLLCHPGWSAGSI*KTKKERERMNL HR**IDRERERERERQIQ*KE*KRINEF EGSKERFTQSVKQRNK/ELEKIRTLDS ETIYLSIYRN*SLRRGQERRTERERMH
12623	26524	A	12749	30	333	KTSYLLPVQWQAQNDNERYSSSKNTIMA LPLPLPVFPRSPSDAERKLDCSAISAH CNLPA\DSPASACRVPAIAGARRHA*LV FGFFWRRRFVAVMAGLVS
12624	26525	A	12750	231	39	INDLL/CLF*FKKLIWGRVW*LMPITPA RWEAKAGGSFEPRSLKQ*AMITPMYSS MGGREQDPVS
12625	26526	A	12751	49	273	HLQVTEVFWFVVCVFFRRWGGSHCV/AQ AGV*WLTGTVPCCSPPELLGSRDPPAS AS*VAGTTGACLAANCRGF
12626	26527	A	12752	505	897	SYLRVQFYSAFSLFFRHEVLPCHTGWNA VV*SQLTTASN/CLGPSNLLKAPHLAN* KKIF*RQGLSMLPRLVLNSWPHMILLP* LPE*LGLQARATAPGSGFTFCLTQDSIL MCSPTVHKLSDSIALETQ
12627	26528	A	12753	335	542	CCNEFFLSQVWVWVMPVVPATR/SAEAGG LPGPGSQRLR*ARSKPVNSHCSAGRCG IDPISIKQKNNNR
12628	26529	A	12754	356	72	WHEYLLMEHTKKCHLS*GLYNGLNN*Q /WCTHPVVPATWEAKAGESLEPRSSRL* CTMITPANSCHCPAWATARSCLNQSIQ SSNNWQGMITGGK
12629	26530	A	12755	340	127	NYLFIYFRDSITMLPRLECSN*FTGSII VHITLKLGLSSLP/ASASQVAGTTGTRH HVQLSNYFKIKIKPKP
12630	26531	A	12756	290	511	KKNQPGT/CGSRL*SQRFGRRLQADHL\ DQLGQHGKAPSL/LKNTKISWALWRTPV FPSSQEAEMEELIEPTSSRLQ
12631	26532	A	12757	254	549	YPGAKKQRPGGDSVRGTHLQSRCWCVLL HNCQ*PKSNTQTFP*PKNLRE*NAT*KS TDL/WPGAAHLCPNPSTLEG*GEWIT*G QEFETSLGNIPRPQIY
12632	26533	A	12758	617	451	NKKRRGLTLLSRLKCNVIAHCSLKYP GSSEPPTSAP*VAGITY\GT*HHAWAY

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12633	26534	A	12759	91	393	KWYTKCECLYLLVSIFSRVLLSIYREVLAQTLGKLSKTMCPALBETVAVNGLQIKSKK*/WLGVMTHACDPSTLGG*GGWIAWGREFGTSLASMAKPCLC
12634	26535	A	12760	10	221	QSHNTNGCLDLHFQKGPQSVGETLNL*TIFLCVCVCVCVCVRHVHM/CYIYSDFICPSIECEYFSFAHR
12635	26536	A	12761	309	55	IIRYKNYISIKLEGWKRLYHATTHEKKVGVAVLISEKVDFRAXN/MYQDKEGRFLL*R
12636	26537	A	12762	640	896	TIVLKC�FVLFCFRDEVLCCPGWSAVA/QSQTQLW*TTQPGLKQSSCLSLSSWN*RHVPPHLMFLKTTFTLLYTCGHLETNIC
12637	26538	A	12763	1	357	IVPLHSSLGDRVKPHLLKKKKTCTSLVIRETQIKITRYTYSNG*S*RKNKAGNNKCWHGYTATGTLIAD/CKSKQMLWKT*QPHIKLNIHY*YNSEIQFLGLYPRDKNIA RCGGLRL
12638	26539	A	12764	129	320	RWKCVCCLKNTGQAWWLIPVIPALWKNQ\AEGSLEARSRLRQ*TLIAPLGYSPLPG*W SGTLSLNK
12639	26540	A	12765	617	435	GVKGLILPKLQKLLKSTIE/I/E*KLPKSFYDASLTMIPKLHKD\RPISHVKIEARILHKISINII
12640	26541	A	12766	243	5	QKIKKRIRKKNQNL*EIWDYVK*PNL*IGIPERGEKVYNTENIFEGIIQ/ESVPNL/AYLVREVDNQIQEIQTTPVRYTK
12641	26542	A	12767	101	16	RTQLFVSVFVFCFLFCFETGSCSITQVG VQWCHLRSLLQLPPPP\GSRDSPPPSSQN RG*NTI
12642	26543	A	12768	362	92	RVPHMDLGEECTSPYMYI*PMTCVFKHG*DGNFVCVTFATIIIIYTI/YLSVCVSI*ICYLVCVYIIYIIYIIYIIYIYKY MKERRL
12643	26544	A	12769	1161	824	QAKDLSTHFTKENM*MG/NKQMKRLSES LVISEMQIKTTMRSHLTHTRITIKMTS DKICP*RCG*MRA/LLQC*WKYKIVSPL WKIVWPFLKT\INMNISCNLMILFLGFY PIY
12644	26545	A	12770	241	237	K*RIWA\GVMAHACKPSTLAGCDGWIA*SQEFETNLSNTGRPCLYER
12645	26546	A	12771	326	6	DTVSRKNKSGKIFQLSSRV*IYERSQSG VKVYKCKTFGKFTQ/HF*AHMRMYTGE KPYKY*ECGKFFILVLLLLMIQKYFHL IKIVRLYLIRKKVSCQPSNKKILQS
12646	26547	A	12772	413	1	KKTFYFFFFETTQAGV**CDHNSPWP*P P\GSDNPLTSAS*MA/GLQSCMHHAQL S*FVFLEAGSHYVAQTDGDSPTSASQSA GITAVSHHTRPILYILIVLSYAISFFSI LYSAYFLQPHLPIHNNFLFSYISSC
12647	26548	A	12773	2	1055	FFFFLRLNLTLPLRLE/CVILAHCNLHF PG*SNPASASRVAEITGSRHQARI FV FLVEMGFHHVSQAGLE/SPDLK*SAHLG LPKC*DYRRDITPGHH*SF**RYFLKTY ISRVL/WCSLLGTFFMFIADFHM*TW*H *QNHFFHLLQIWKLISERLRSAGGQOAL KTVTSTFSSKYVCRAFLAEPGWIAILYV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TF*SLDSRRTCLVVAVSNFFYSTLFLKL RQQVLLTG/PYHLFSARPSSCGSDKKAR ELNLSLSL\CFFFFGKRVSGTQAGVQ*H DHSSLQLWPSRLKQCSHLSLLSSWDYRS ITPHLANF/CNFLSGWSRTPGLK
12648	26549	A	12774	315	98	FRCFNLNSINPLESPHVRKTCAGRAQWLA PVIPPFWEEA\SQMPQVIHSR*LEARS SRPAWPTWQKPCCLKYKN
12649	26550	A	12775	275	59	NPSPYKIQKISAWWYMPVVLATR\RLQ *AEIAPLHSSVGDRAKPCPKKQKTNKQ TKTSGEPLVVGQPATVC
12650	26551	A	12776	73	381	SLNSELSSIPRPTWESPSTSDSAWPMQ NLASEPLPLP*TTPPDPFALSA/PE/P LPFTPSPRDTLPPPLSPSYKQAPVLSVH PFVMPKLYVPSSPLLLSFLYL
12651	26552	A	12777	274	342	LNCVIA*WLMPTIISALWEAEVGVSA/P /RSLRPAWATW
12652	26553	A	12778	2	478	TIYYTKYTTFRVPLNLGLQLLTAFFCVCV CVSLNGFKNAKDYGGSHLKYSVYITGFL LQFSLKFDCFLCVCVCVFP*MA*KMPKI M/RGSHLKYSVYMT*FLF*FSLKLKYFC DFILRKRI/WPGAMAYTCNPSTLGG*GG QIT*AQEFETSLAKVVKPCIY
12653	26554	A	12779	680	453	SETDWRKNKFFPSNFPNLRNLSWTNSC SKKTFKKH/RVGLGVLATCNPSTLGG GGWSP*GQEFENSLTNMNVHFS
12654	26555	A	12780	59	487	SLHKKHPERGLQSFQGCWTEMLGGSHVQ QRAWELCAPNLTCPGYLSFFLRQDQAL LSKLECSGTIPAHRNPSLSPQLKVSSH LSFPSSWNSRCTTPHQLLLFF*DRIRL FCPSWSAVAQSQPTVT/SSLPSQLKVS SHLSFPSSWNSRCTTPHQLLLFFNFL* RQVFTMLPRLVNS*VQAILPPWPPKVL RLQA
12655	26556	A	12781	109	361	LSPWHHSRNYTLIYPYTLNFWMSAFPTP KEFFFFSFPETRPHSVQAQAHW\AIIA HCGLDLLGS\SDPPTSAS*AAGTTAII PG
12656	26557	A	12782	3	204	LIDGSLALSC*LFCGGATIAHCSLELLG LGQ\SPVSATRVAETTGVCHHAQLAFVN LHLRTRSKHCGH
12657	26558	A	12783	2357	6366	LTGS\NSHTTILTLNI/NMGLNAPI*RH RL\ANWIKSQDPSVCCIQETHLT\CRDT HRLKIKGWRKIYPSPMGKQKKAGVAI\ LVSDKTDNFNPTKIKRDKEGHIIMVKGSI QQEELTILNIYAP\NTGAPRFIKQVLSD LQDLDLSHTLI\MGD\FNTPLSTLDRST RQKVNKDTQELNSALHQADL\IDIYRTL HP\KSTEYTF\SAPHHTYSQNWTTIVG SKALLSKCKRTEIIT\NYLSD\HSA\IK LKLRIKNLTQNHSTT\WKLNNLLNDY\ WVHNEMKAEIKMFETNE/NKKTPTYQN FWDFAKAVCRGKFI\ALNAHKKQE\RS KIDTLTSQLKKTREAKSKQHSKARRQE ITKIRA\ELKEIETQKKTLQP\LKKISE SRSWFF\ERINKIS\RPLARLIKREK NQIDTIKNDKGI\TTDLTEIQTIREY YKHLA\NKLENLEGMDKFLDTYVSLPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LNQEEVESLNRP\ITG\SAIVAIINS\LPTKKSP\GPDGF\TAEF\YORYKEELVP\FLLKLFQLEKEGILPNSFYEASIIIPKPGRDTIKKENFRPISLMNIDAKILNKILAKRIQQHIKKLIHHDQVGFIPG\MQGWFNIRKSINVIOHINRAKDKNHMIISIDAEKGFDKIQQPFMLKTINKIGIDGT/YYFKIIRRAIYDKPTANIILNGQKLEAFPLKTGTRTGMPSLTSPLLFNIVFCPIVFWAR\AIRQEKEIKGIQLGKEEVKLSLFADDMIVDLENPIVSAQNLLKLISNFSKVSGYKINAQKSQAFLYTNNRQT/EEAKS*LMS ELMSELPFTIASKRIKYLGIQLTRDVKDLFKENYKL\PLIKEIKED\TNKWKNIPTCLWVGRIS\IMKMAIL\PKVIYRFNAIPIKLPMTFFTELEK\TTLKFIWNQKRS\RIAKSILSQKNRAGGITLSDFKLYYKATVTKTAHWYQNSMVLVPKQRYIDQWNRT EPSEIIPHTYITILI\F\DKPLLEKNKQW GK\DSL\FIKW\CW\ENWLA\ICRKLNL\DEF\LTPYTKINSRWIKKKDLNVRPKT IKTEENLGITIQDIGVGKDFMSKTPKA\MATKAKIDKWDLIKLSFC/TICTAKE TTIRVNRQPTKWEKIFATYSSDKGLISR IYNELKQIYKKKKKTTPSKKWTK\DMNR HFSKE\DIYAA\KKHMKK\CSS\SLAIR EMQ\IKTT\MRYHLTPVRMAI IKK\SGN NRCWRGCGEIGTLLHCWWDCKLVQPLWKS LWRFLRDLELEIPVDVPIPLLGIYPED YESCCYKDTCTRMFIAALFTIAKTWNQPKCPTMIDWIKMWHIYTMYYAAIKNDE FMSFVGTWMKLETIILSKLSQEOKTKPRI FSLIGGN
12658	26559	A	12784	787	926	PQAIRRPRPPKALG*HNSVDLGWAWWFT PAIPTLWDYTHEPLYLAKIS*CFKKVYKFVLNCIQNCPGPHAAHS/SGKTS*V*SNYLFFSFCFETKFCSVTQARLQWHDLNS LQPPPPGFKRFSCLSLPGGWDYRRLHTR SANFCIFSRNRVSPSWPGWSPTPDLRRS AVLGLPKRWDYRREPPCPAKIYTIMAPQ KVNSHSSQPVSFSL
12659	26560	A	12785	248	285	C*VIF*CVMIYVLIYVEKITSIRLAVY VV/CIIITRLFVK*ICSCLLGC*FLFFNV C*LYIFIIFVFFFFFFFVFVFVFELN ILY
12660	26561	A	12786	243	37	RRSAGHGGSCLS*SQYFGRPTRADHKVRS N/RGETLSLVKIQKVSQAWW*EPVVPAT RQAEAGADAWVDR
12661	26562	A	12787	75	289	DYRHEPRFFFLYTTFFEMDSHVARAGEH WCDLGSL*PST\*GSSDSSASTSR\QRH HAWLIFGFL*RRGFAC
12662	26563	A	12788	83	256	RKMYVVGLEFVTAQN*K*PKYPSTEE/YI K/RLWYLHTMEYSAIKIEKLGTRAQNR LILY
12663	26564	A	12789	197	499	QSLKSVEETVFRNNKQ/SIPTFQVILMP WWLIPII*ATWEG*GRRSPNLPGV*DQP QHSKTPSLQKTKFS*AWWRVPVPA\ IGEAEVSGIPLSPERSRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12664	26565	A	12790	394	91	FYNSTKFKWKNIQFLITRCRGDQIQVIR AHAVQLGFHVIYF/CLSQLNSIYLYISI YVYTYRYIHTHMCIIH*YLYIYTYIVI KH*KEHWWIKHCFPTERK
12665	26566	A	12791	735	75	FFFRQEGFLSPPKRGVPPPHTKKYFSP RGSFLWGWGTSRPPPRKCFSPPPPVFL PPPKKKKIISFSPTKLAPPPEYFKSPPP PS\PPPPSSPSPSTFFFKNFPSPSF SSPPFFFPSPAWEDPPVQSRRIY*FLPP PF*IPETPR\RVLKKKPGEGRSWGLFPP PKGPKRRVPLGPEFKTRLGHKTKPRFFK KKKKKKRFLISCLWWHPAIPSTLGG
12666	26567	A	12792	482	342	MGVFVFFFTGSHSSVTWAGVQ*CNLSL LQP/PASSDPPTSDSRVAGST
12667	26568	A	12793	405	169	FYKKKKTGSGLALSRLCSGTIIAHCN LELLGSRSLRL\SNTPTLAS*AARTVSV CHQTHLIF*FFVETGSCYVASA
12668	26569	A	12794	270	94	YVCYSYKQIKICSHVKRRE*NTFKIYLL KYIALGLTGHHFPL*TFSTVTLWPGAV AHACNLSPLEGQGRWII/R/QGEIKTIL ANM*IPVFLHVNIFLSVCSYSIHTLDY LFYYSYCYLISL
12669	26570	A	12795	284	415	NFIKIIKKKVMGLFYGKTFLLNLKKKKR KKK*WPGTVPHA*NPST\LGGLGGWITR QGEFETSLATN*NPTKSISRGF
12670	26571	A	12796	1387	32	APSSFAIRSFFSGPMNAFFSSMVWKRFP PNLEVVMNLRISFRARRFVCTSKDLR RVSTRFLVHLTAFLGYKAGMTHIVREVD RPGSKVNKKEVVEAVTIVETPPMVVGI VGIVETPRGLRTFKTVFAEHISDECKRR FYKNWHKSKKKAFTKYCKKWQDEDGKKQ LEKDFSSMKKYCQVIRVIAHTQMRLLPL RQKKAHLMGDQVERGAPVPEKAD\WAPR EALSSKVLVTQVFWAGIK*SNFIGGDPR AKGYKGGQPVCWAHPRKLPPQRPHPRAL RKGGPVLGAW\HP\ARVA\FSVARRWGR KGLPFHRTEINKKIYKIGQGYLIKDGKL IKNNASTDYDLSDKSINPLGGFVHYGEV TNDFVMLKGCVVGTCKRVLTLRKSLLVQ TKRRALEKIDLFIDTTSKFGHGRFQTM EEKKAFMGPLKKDRIAKEEGA
12671	26572	A	12797	86	364	EQDNRIFFSFLSLFFFGETEFGPFAQG GGQGAILGLPKPPPRGL\SSFPT*GSQE VGTTGAPHDIFCFNKKGETPRLYKKNK NNRGGGATP
12672	26573	A	12798	101	440	HCSRYATGIFEWYSGLVLILLRFGIYE PMNLNIGDPYDSPSRLYKMRLWERMAK SLIEVSLKNSHFWLGMLAHACNPRTLGR IGGRIA*TWGF\KTSLGNIARPHLYLKK I
12673	26574	A	12799	364	195	NPPGDLGEETLLWGGEIMGTTPP*FPPP KEGFLPDPPGGFNSPPI/QGRSFSFPP PGKFGPPQGFFKRPFFFFFLNNNQ
12674	26575	A	12800	86	489	PTAMAEEDIAAGGVMDINAALQELLKTA LIHDGLAHGIRKATKALDKRQAHLCVLA SNGDETVYVKLVEALCAHQINLIKVDD /NKKLGEVWGLCQIDREGKPRKVVGCSC IVVKDYGKESQAKHVIRENF*CKK



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12675	26576	A	12801	64	211	GNHKKSNYS LAPWYTTVPAT*EAEAGGSLE\L*CAMITPVNSHSLA
12676	26577	A	12802	300	3	NNVTTGSNIQFHSFPLIRKIDICVSYIKNDANNYIKNSNPNGETQVYQ*YSFSN*NLKIWLKVA\NPSTLGGHGGRIA*A*KFKTSMGNIVTPCLINKQK
12677	26578	A	12803	208	394	SQHFERPRREDCLS\QEGQYSEIPSVQKNVKISWAW*CMPAIPATREAEAGGPLEPRRSRLE
12678	26579	A	12804	183	348	AFILGKGKYEYPYNPCLGWA*WCMPVVLA SWEAEAGG\SLEPRSSSEL*CAMLIGCLH
12679	26580	A	12805	397	238	ETEFPPCCPGWKWGDLSGQQLPPPGFKRFSCFSLPSK\WGQ*SLAPVGKGCK
12680	26581	A	12806	1	293	PTRPRTSYEKQGYLLLPVFSIVLEVLARAI SQETELKSVQMGKEEVKLSL\FVCVYIYA*ENPVESTKTVDANLFDTRDWFHALFPQTVGEVGMVLG
12681	26582	A	12807	297	281	AKNPRRQPREIPGGVFPTPGFPPYFKAKMPEGFPFGGFFFKGGVLWGTPPPFFFFF FFSETESRFVTR\LQCSGAISAHCKLRLPGSCHSPETC**R*G
12682	26583	A	12808	255	59	AGCSGSQLEFRPRGV D H L S P G V * D Q S V Q H G E I L S T K N T K I S W V W S V P V V G \ E V G R S L E P G R * R L E
12683	26584	A	12809	247	310	PLHSILGTPTTPAPTGPGLLIRTSILY*KPILSQAWWCAPLVPAQ/EAEARGSL EPRDSRRS*AMIKPVNSHCTPSWALPRP LPQPLESHC
12684	26585	A	12810	101	477	IGKEEIKLLFPDNLMEYTVNF*MYKPL ELIS*FSKVTEYQVNTK/SNCIYT*QL QIENEIAKTI*FMIASKSIKYLKISLTK CN\KWRDILCICIGRLSIIKVLVLPKLM CGGEKIFNPNTGFW
12685	26586	A	12811	1022	696	CFVFLFFKEMGSHYVAQAGVRWCDHGSL YPPTP\GSSDPPTSAS*VAGTIGAHHT WLIFKFFVETRSCFLIQAGLKLASSYP SQPRTSPKCLGFTDVKSLHLAWLCP
12686	26587	A	12812	166	143	RKEERFQINNLFHFVEKLEKEEQI\NPK TNRKKKIKTRV*INEIYRKTIGK\IN KNKSWFF*KINKIDKPLAMLDGRRDSN Y*NITKSIIEGRRRKEEAGKRKEEGRKR RRRWRQRWR
12687	26588	A	12813	163	423	KAFWEFINHKKTGPF*RGPIGKVSPPGG N L A S S I * K G / D P F P S P L K G P Q G S S G G P P P K K P P T G F N L A F G G L R G R E T K R G P F F L A G L L P
12688	26589	A	12814	2521	2842	INTMYFPP*EMLVGWAWWF/RASNPQHF GRLRQADRLRSGVRDQSGQHGETPRLLK NTKISWAWWRAPVIPATWEAEAGESLEP GREGCSEPRSCHRTPVWVTRMRLY
12689	26590	A	12815	173	395	LDQPGQQRETLSLLKKKQTNKQTKKKNG FKKFL*LDTWVHTY\NPTPLGGRGGGFF *GQDFETLANMGKRGFY
12690	26591	A	12816	43	346	CVYVS/GVCVCVCVCCLASVCMYVCLH L*VLFGIFYV*DHNICKLRSFCLFKNT FSHVYF*KIWPVEL*VTVFLFLSSLL HTSCVYEKSYAILIFSAL
12691	26592	A	12817	647	931	SQHFCRPRADHLRSGVQDQPGHHGETP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PLLKI\QKLAGRGGGA*L*SQLLGRLLKQE NRLNPGIRSCSEPGSHHCTPAWATE*DS VLKKKIGADKY
12692	26593	A	12819	392	2	PLFFFFFFFLETESHVSQTQAGVHNPPGP SKPPTSAP*AAGTTGMHSAHAQ/LIFF L*TELPSCREPGCSAMAVHRHDPFTDQHG SASFLIWASSPLLRQTGDSSLLGGHHVD AKFSVDTQLALCTKAQNS
12693	26594	A	12820	1183	870	DRVSLTTPRLGVAVARNLAQWKPLPPGF KRFSCSLSPSSWDYKHTPTPG*FH/RG *FFVFLVETGFRHASQ\AGLNSLPQSDP PTLA/FPKCW\DYR\HDHLAWPRKM
12694	26595	A	12821	172	298	IYLSIYLP/ILCIHLSIHPSIYPLYL SINPSYWVSFSREL*LT*L*YLSIYLP IYVSIYLSIHPSIHISYPLIHPIGLF LENFD
12695	26596	A	12822	51	254	YDFLKKHLLSSYRAKDLESFLHLHLHF SGN*SVSYICVVCVCVCICVCVYICIL IKSWCS*S/CGVL*AICAGVGWC*LIFG VL
12696	26597	A	12823	199	668	QPLPAPSPSAQKGRAHPTSPARPQAE/ SLPSQSLGTRTRPPLGRPP*SPPWGQVD LWGWLGPSPTLPAPESLPASLSTEVVL CGTRYLVWGRSGAGQA
12697	26598	A	12824	33	442	GRGKLLKKSQKQRKNALLKYDSKTRVGT LEHWTSPVTRPPLL*INIRLIKLDVIK CSIHKIFHSEFLFFKQHSGL/CI*LSK* LCS*KIHQSGLGTVAHVCNPSALGGQDR RIT*GQEFETN*VNMVGPCLYPPLPP
12698	26599	A	12826	363	75	HWEPRPAGPTLPAPGSESGRCPPHHTT SG/PPPPNTHTPMSRSPWSWEGSDQRPO PHHTDTGSPEN*GSRLRHERPPWGRERQ RPPPTTLVRPLSH
12699	26600	A	12827	76	486	CTVNLFTYFEMESCSVVQTGVQWCDLSS LQPLIWFSCVPTQISS*IPMCCGRDLVE GP*MMGAINSFLLCCSYDSK*VS/ARSDL FFFFFFF
12700	26601	A	12828	345	672	KMKCTADLSLLEKDT*IKLEENR*QERI MLRAEVNEIENKIENKNTGGSSSEKYY- KIDNPLTRSIRRKVN\KITSIRNEKGSV TTNPTEIKRTVKEYIMKNFMPINLT
12701	26602	A	12829	208	1	PSNSTPIFKRNENICPHKDPCTLMMLAA LFVMSKK*KQLKCSSNDE\KLWYIHMME *YIAIKRNKLLI
12702	26603	A	12830	649	172	FPLKYSLSSTSVMAPSFTSCGGSQQVLL APLSRLLAWPNV/HPPPPQPRHPAPHSFL SPPRSPPNYSP*SSQGPLLQPQSKHVRP LPQANARLPSAKNPARGPPGAAQAPRDR PPA/VCPLPPHSPLRHERAPRFLPLP ATEPAALHAVHPGRRQERV
12703	26604	A	12831	1068	667	KLSWFFCSRLRLHFGSIFKVPSP/LPVPK LLLPIPSLCPSLPLQLQPAQVPFNTAT WLCFC*/P*RV*PAPGYQVRVGHFNFFPL QLNFIPILQ*HLGF*KSASLSSSSSPK KVSLLCHPGCSAVVRSACNLKLLIS*SA CLGLPKC*DYRLQSPRP/PTIFKVTM CLLKSLTGVSF
12704	26605	A	12832	268	1	KCFFLLALNWPEFILDYFILNW*NSLRT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VTEKFLFMTLFLTY*NMNRPGMVAHACNP S/TLGSGGGRIT*AQES*TS LGNIVIP CLYQKL
12705	26606	A	12833	654	321	LVGIRFLKVKYFNIFKPHLLAITSPSLE VFNLQHFIYIFLLFIYF*ETRSCSVAR LECSGVIIHVCSLKLLGSSNPPALASQV AGTTTAHHCAQQHFCCILEKSNLCITYFPL
12706	26607	A	12834	867	201	RQMSPTRLRTKS RDVASRSSFSAWAWGKL FTFWDFMSLSVLQGPGGFHSPQP*TQ GR*VENNQEPLATPFFGPERSLPGQPR LEPAHSGKKRRGLPLEIRPPVNVSDIHGDP SGAQWLVRGVEAGPWAVGGQAP*SEGSP PSPPLDVSPD PGSSLPRSSSP*MDLRA* LSLTF*TFQKGSGN/DPASSPA\GKPG* EWRLIKGPPQGLLLGPEMWGSQARVLS
12707	26608	A	12835	328	1365	YAFCLMMLDKKQI*\AVFLFEFKMVHKA AKTTONISNTFGPGTANKHTVQWWLKKF CKEESLEDEERDMGHGKVDNDPI*EP\Y *TT*KITEELSVDYSTVIRVVQHSKQIG KVKKLDKWVPHELSGNQNYRFEV*SSF MRNNPNPFLNRI VTCNEK*ILYN/RPAQW LGPRGQLQSQFPKP NLAPKKKRSLVHW/ SPVGL LAPILDPTYSFLNP/GGETITSE KLC SGKLGKMHGKLYLLPALVNRKGPI \LLHDNT/RDCVFAQPV LQKLKELGYK VLPHPYPSPDLS PSDYHFC*HLDNFLQG KH/SQHGAENAFQE FVKS*STDFYATGI NK/LFSHWQKCVCDCNGSCFD
12708	26609	A	12836	7	328	RRERERERERERERERERERERERERER ERERERERERERERERERERERERERER ERERERERERERERERERERARV*EKST RYKSPPPRIPLLR/RRV*RKH PHARAL SFFLYKKTGGERAPS PVCVGKFTW
12709	26610	A	12837	219	350	PFNHTYATWSII ISNVQVCFMRAQDIYL LIYLFEAGSCSVA\RLECS DMIMLHCSL DLPGSNPPISAT*I
12710	26611	A	12838	189	359	LGLDGVMRVGPCRALGPS*EEKSSRVQW LTPVIP A/LLBAEAGGSPEVRS LRPAWP TW
12711	26612	A	12839	368	77	KNPNFLKFGSKPMGPPIYSPP\LEG*AG GFINPGF*TPPGYM GKPPFLKY SNLPG LAAPGGCSPFPGGLGRKISFTPMEVSI NPGSPLSLPPGEQN
12712	26613	A	12840	16	173	KTDVHSKCTKRLFTAALFLIVKKWKHLK PP*VD/EINKMWYNHIVEYYLAIKS
12713	26614	A	12841	425	45	NSFVFFFFLLENRVLT PVPARLE\CTGV IL/APHCTL PALPEFKRFLVPSALLSSW DYRPVPVMPWLNFCIFVETGFH\HVAQS VLKLVSLKL/PSPTWDV PKC*DFRYSVR CCGLFF
12714	26615	A	12842	237	375	LLL VVVYILKKLW\LG VVAHACNPSTLG GQG GWIL*GREFETSQVNM
12715	26616	A	12843	21	325	TSFFFLESYSVAQAG\QWCDPGSLQPQP PG/SQ/DNPPTS G*VAVTG/MHHARL IFVFFCRDGILLYCPGRSKI IFSSCIRE LFKKISDFLLTMLIFCNSNKG
12716	26617	A	12844	369	58	PISPLOFMLPFLKNQSPYGF FFWKKNF PPPFLGGAVLKT PGF*NLFKKIORGFPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PFPKKKKPRERPKPCPPKFG/SPPPFFYPGFPPPKKGPPPPPPPPPPPP
12717	26618	A	12845	211	409	NALKPKIHFFFSGGGLKGIWVGNTLLDIGLHKTFFF\*GDFYYAL\*I\*AENALFGGGDCAPHLQVK
12718	26619	A	12846	200	33	QKTNNTKCWQGWGATGTLIHF\*GEFTRVQSHWKIVWKFL\*/SLNILP/SSSSSSSSSSSSSSSVKNLCLHKACTWMFIAALLLAKTWKQP\*CE
12719	26620	A	12847	416	125	KIPTRPGKGGPPLYPRPFRGLNKQIGLTPEFGTPLGNKGKSFPPFQKNKN\*NWPRGGPIGPPSPGG\*VGGLTLKGEVSTKLDSPAPPFGGQKWPLP
12720	26621	A	12848	85	397	KIHIFFFIFLVSLKGLSFLLTFSKN\*VF/SFIDFLILCVVCVCIIFYCFILILFHYFCLFGFCLFLMFVS\*CQSLDFYFNSF/YIF\*YKIQCYKF/CILIF
12721	26622	A	12849	1	246	RPRRHLVASLVLTLQNLGSSPLPIKIISWAWWLMVPVPTFWAEVGGLEPRSSRQ\*\*AMI\*SPCPPAWAT
12722	26623	A	12850	161	1	NKTTSSQIW\*PMPIVSTT\*EAEVGGSLRPRS/L/KLKCAMISPVNSHCTPTWTTK
12723	26624	A	12851	65	244	STYYLHSLPFLDISYKWNHTTC\*SRYFMGALFLIAIK\*KQPKRPSADEQI\*T/IMWYIYTLEYDLAIKRNEILHAATWMNLKNIMLSKRSQTQKT\*HVV\*FHL
12724	26625	A	12852	235	34	TTIAVSVLILKELMEP\*TLQPDFLG/WSLITESVDHVQWHAPVIPALWEGEVEGLLEPRSLRPAWATW
12725	26626	A	12853	168	453	CQLRGASGTQGGPLSBSQCQQPCP/PECRPSKPRPCGCRI\*SPARTSPQSPASMAALPTNERTPPPALKW\*PK/CPKQSPQSAKSKSPVKSTERTAK
12726	26627	A	12854	244	3	ELQVYMHIT\*IYI/C\*SIYTKANIYIKYMHMCVYIYTHTHVCIHLHIYLLRHGFGCWLMLGKVRGCEGMAGLMKAQQCWGW
12727	26628	A	12855	376	428	KWEPGGHTSFFFFFKGLVLNFGRGVLQKTRP\*GGGQGGKFNPNFSGPREPPPP/PPPGGGKKGPPPPPGVFVFVFEKGGSPILPRGVLNPGAPKGVYTQRGGIKSGNQGATPLSFFLKVWF
12728	26629	A	12856	129	395	APPNTHPFLSEAPQSLSLRPPSPAPSNSSSR/PPVWRASQTHPPQDWSSHCSPPWGAPPQI\*PFSDSLAHPQDWSSHCSPPWGAPPQI\*PFSDSLAHPQDWSSHCSPPWGAPPQI
12729	26630	A	12857	363	97	GLATLRLVSNLSQAQVIRPPQPPEVLSLPKC\*DYRPGRPASLIHVNSRQT\*KVAP/CSKPLAAAAHQSGPATETTRCPSRCGPPIF
12730	26631	A	12858	322	361	KSEKQS\*VMLAVCTLDMMKMT\FISVVF LPKTHN/LMSNYKKNTRQIPMEGHSTIYLTRIPQNCQGHQKQ\*KSEKQSQQESKKK
12731	26632	A	12859	88	417	HFTFFFFFFFFFFKRCGGFFSPRLKRLGKNFFFLDPPPPG\*RDFSPSPFKEGGF\*KP/SPPPLVFFFFFF\*KKKGFPPLGAGGF\*TSGPGETPPLYSPEVWFFYGGTGPPTPFFF
12732	26633	A	12860	217	2	LILINKLANMHCFVVFETSLT\*AGVQW

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						HDL/GLLLRLAPPRFKQFFCLILPSSWD YRCALLHPATREDEA
12733	26634	A	12861	375	145	LSFFFFF*KPGSCSVAQAGVQWHHSSL QLQTP\GFSDSLNSAFSVARPVVHCHT RPLSPFNICWRARPKQKVFL
12734	26635	A	12862	525	852	NLLSIYFFETESRSVAQAGVQWCHLGS LQPLPPRF*IKKPSNTALEM*NLLSIYFF ETESRSVA\RLCSGAILAHCNLCPLGS SDSPASTSRVAGVHHHSHLSSWDYSCAP PCLANFFVFF*VETGFHVVSQDGL/DTS *PQVICPSRPPKVLGLQA
12735	26636	A	12863	3093	204	EPDKTGPVLWKVGGGARVPGMAETLSGL GDSGAAGAAALSSASSETGTRRLSLRV IDLRAELRKRNVDSGNSVLMERLKA IEDEGGNPDEIEITSEGNKTSKRSSKG RKPEEGVEDNGLEENSGDGQEDVETSL ENLQDIDIMDISVLDEAID\NGSVADC VEDD\ADNLQESLSDSREL\EGEMKE \LPEQLQ\EHAIEDKETINNLDTSSEDF TILQEIEEPSLEP\ENEKILDIL\GET* RSEPVN*ESSELEQPFQDTSSVGPDRK LAEEEDLFDSAHP\EEGDL\DLASEST\ AHAQSSKADSLAVVKREPAEQPGDGER TDCEPVGLEPAVEQS/SVAASELAEASS EELAEAPTEAPSPEARDSKEDGRKFDFD A\CNEVPAPKESSTSEGAD\QKMSSPE DDSDTKRLSKEEKGRSSCG\RKFLGLVG LSSTTRATDLK\NLFRQIWGRVGGAPRL WTNARSPGSFAVYGFVTMSTAEATKCI NHLHKTLEHGKMISVEKAKNEPVVKTS \PKRGSDGKKEKSSNSDRSTNLKR\DDK CDRTDDAKRCDDESVEKSK\DKNDQK\P GPSERSRATKSRKSRGPKRTVV\MDKSK \GVPVISVKTSGSKERA\SKSQ\DR\KS ASREKRSVVSFDKVKEPRKSRDS\ESHS RVSEREREQR\MQA\QWEREERERLEI ARERLAF\QORLERE\RMERERLERER MHVEHERREQRER\HRE\REELRRQOE LRYEQERRPAVRRPYDLDRRDDAYWPEA \KRAALDERYHSDFNQERFHDHFRDR GRYPDHSV\DRREGSRSMG/SIREGQH YLERH\SDPEPH\QQDSLRL*LGWGYEL* Q*RLS\EGRGLPSFPPGAGRDWGDWLE DEDDPVMGKGTAERGPMMDR\DHK\RWQ \GGERMSGHSGPGHMMNRGGMSSGRGSF APGGASRGHPIPHGGMQGGFGGQSRGSR PSDARFTRRY
12736	26637	A	12864	2	456	IHLGSGSEGDGSSGGLGRGNSNTSRFSS SSWARGDNVPRPPPPAVCSWISEGDVQN PGLGEAGAGSSTPGDGGLRY/WPGLLG A*GRGIGGDDDDLRTLGLAGVQQCGKG/ RRGPRGPGRGQEPRRPRDLGLRGPRRAQ GAA/SATAAPPP
12737	26638	A	12865	388	1	LIKMTKVKKTAITKC*RGWGRTGAFIHC SWECKMIQPLWQTWVQLLKKLNLYL\WK QPKCPLM/VKWIKKLYISMDSYSAVKKK ETLMTYTA*MTLEVALLSERSQTRKGER GHILWDSIYINFQMQTNL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12738	26639	A	12866	198	3	KKQKQTKNPPKIS*ALWCVPVVPATWGA KVEGSPE\PRRSRLQ*AMITPLHSSLCN RVTRGRTRG
12739	26640	A	12867	415	973	NEVNCAQFSLLPTEYMGHRVEGATGHG TCPSVPPNTHLHTGWCLQHHRSRAWG RGGSHTHRCQQRVPDGEHP*YIYIAVHGE PP/ESPPQPSPLSCPPQGNIALREPP QGLPLPGTLP SHPPPFWHICKTHSSES RHPFFPGFCGLELEKGVDFIHPPLTLP KLPNPLKPEPTPTPQTHI
12740	26641	A	12869	715	893	PCVAPHSTREERFRLTSESTNQKVLWWG ID*T/VILILTGNWQKRHLKSFFLGQKP GGMAP
12741	26642	A	12870	342	58	KKKKPKENEQSIWDMWDFRTSDI*TTG VLEEQFRE*GRKIIIFKEIVRENSNLTK /QINLLTQEV*TTT/HKNMNKSTPIHII IKLMKTTTKEKI
12742	26643	A	12871	110	401	SFYSVMILKASRIVICLET*LYAYIHTL YIYTLCTIYYAYVNIYICTHI\NIHII HVYTYIYIVASIYYSMSAWYNIKVS KDRQTYENIALITYY
12743	26644	A	12872	439	256	SYFMRFGGDKISKLYQFILSRRWKQSTC PSMDEWINKMWH/ITIMEYYSAK*RNEY SYMRHE
12744	26645	A	12873	356	43	GTPERHSHSHSQSGSPIIGAFMGIRASV YSLSCVLLMLSPQRVLFYFSAFKQQS \WSGKVAQAYNSNTYKAGSIT*GQEFK TILGNIARPCFYKKKFLANS
12745	26646	A	12874	341	205	REIKKMVLNKKFFSLQFLGKKKNFEFF LKKKKKVKFAPPVFQF*VPIF/CSF*KK KVFGFFFSPIKIFFFFFFFFETESTSV TQEFNGTILAHCNLGLQGSSSSPASAF* VAVSQDCAIELLGDGRRLCLEKKKKKKK KNFGGKKKSKNLFLLKRRKMG
12746	26647	A	12875	474	206	PIRANGPVFSPPPPPAPGTCPHPLVIM LSRHLRQSHPTTVQPTSGLLPSPPA* LSLETQHFKTAHFIFP*H*SSGLGPGWG SPVGEPPG/HPKLCQPAAAAEAWPPRE GTKARRHEGLPPAPCAWGPAPRDAGSRL BFPTLPTIPVSQSPGR*HGAGGRPSCLR AFVPSRGGQASAAAAGCRQSFGLALLP LGSPILGQQNFSARGR
12747	26648	A	12876	257	467	YRVFTLLPRLEYIMAHCNLDLGSSDP/P QVAGTTLK*LSRASRVAGTTGVHHHSWL IFK/YFL*RRWRRFSL
12748	26649	A	12877	867	1409	GPTVLVGGQDWN SVLQOPRAHSFTPRGG AGGLGGGYVLHKPIPFSSQELLGAFPCQK QYRVPPPLEAQLLRQARSPAFIY*AAVL CQAQGPSPSPCSPMVSPRPSGRAPHLGA APQSGQKALASTSSPDAEPV/SVG*WCP SNPALQGGQNGAEPRAVSITSGALSLYD CFLDGWWEGRSLGP
12749	26650	A	12878	1416	740	IRNPRWVQLDVFAAAPMGRSSPLFLLLF SFLKTVLRGSMIPSTVPS/FHKGPAACL YSLSLRS*SQAAPSPAPSSSLPTPSHPG LTQPGRGRRKADIS/CSHSAFYVP/SL PHLPWACPLSLPQPVLFSLFCFVLF*D GVLLCHPG\WSAMARSWAHCNLHLPGF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QFCSLSLPSSW\DYRCMP\GLG*FLEF *VEDGGFTILVRLIWN*PQVIHLPQPP KVLGLQA
12750	26651	A	12879	961	31	PSPVRDSCVAWAGERRGLGGSGVWRSH ARGPGLMRGLPASEPAPCVLGSRPCFRV AFETPWTSPASCMFERCPLWRPPALVAA GLDPFLLSSTLTAVCPDLIRSWKKGC DVCDNRNCWSTHSPACRDAILAPILAG RGEICGLWG/AAAAGTGRV/TPVSGLTF STVDFDSSARG/V*GGLPRSTGGPRVRG PGQPVPLPGLPAGVALAPLEGRPQEPAP ALSHSLTGSFLGAWLCGCTRHGRAPVL LEVSIACGQLCEAAPQIFIQPGLQQLP TPSATSPAYLWVDVLLTLPVVIKQKRV SFLTKE
12751	26652	A	12880	232	28	PALWVPVVARFDGMEETGQNHWSKEKAW PGAVAHTCNPNTLGG*GGH/MT*GQFEF TSLANMAKPRIPP
12752	26653	A	12881	331	1	KNGPFFKNPEFFPPPKWGVPPNPPTFYF PWPEPIF*LTPGPLKKQKIPFQ\KGEIL GWGGKMGNPLPFWKWGGPPRESKSSPRF YKTPPPIFKKKKKGGSSRSRTSPRV
12753	26654	A	12882	370	287	VSILAGCCGVAMIDNTVLVHKEVKILRK *IIKK*CI**FRGHSK/HNFSG*AWWLM PVIQHFRPR*GSLEARSLRPAAWTQD PHLYEK
12754	26655	A	12883	656	1168	EPSRGVWPHEHDARINGSKKKKSKDKKRK REDEETQLD/IVGIW*TVTNFGEISGTI AIEVDEGTYIHALNGLFTLGAPHK/ER IALKPGYGYLSINSDELVV/GRSDAIG PREQWEPVFQNEVRNGGPAEMGEKRN GTKWREDTDHTSFPLFPSTGGQPKAHNS WRKVCH
12755	26656	A	12884	205	452	ASGSAHRFRFTSFETGRVLDKPSQTDHT NRKRGGPVNVK*SFL/WLGAAAHACNPNT LGGRRRTA*AQEFRTSLGNTVRPCLY
12756	26657	A	12885	112	290	KYNIIQYNIVFSCHDPLVSFNLFFFFFFF GKGGFPLSPRLKARGRVWGYLNPPLPGK RNFWAPPQGFEEKGLPPP*SPPFGGVG QAKNLGPGFQPPAPMGKTPFF*KNQNN PNWGGQPLNFKTLGGGGPKISF/PPGGG GLNNPKPSPGPSTWGKGNPLSQKKKK KD
12757	26658	A	12886	406	190	TRSLARGGFGRPLQKPYWNEQSFTIMAKK \YEQPKCPWTDKWNKMSILTVG*YAA MKRRDVLTCATITCR
12758	26659	A	12887	440	160	RVCVCVCVCVCVGVFVCFALWLSLIYN *VYLFLFVHNLGRVSFSYFLNLI*FFE VNHV/HNYVQMIQNTKLYLKSYLETFH/ CPC*FPPIILH
12759	26660	A	12888	201	411	HIWDVILIRHALGNFLTISCIYIKIWL DAVAHTCNPNTLGGQGG/WIT*SQEFKI ILGNIGDPLSTKKNK
12760	26661	A	12889	138	464	SCTMNPSEMQRKAPPWRWRHS*APSTH KMNRMVMSEQMKLPSTKKAEPPTWAQLK KLTELA/TKKKSLENTRGTTQTSKNMLFA ALMIVSTGCAGVPSSSKETATIEDKP
12761	26662	A	12890	146	366	FSVSMKYFV*IH*FYHL/KLLLMVYL*Y

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						GFLAINTSQNISCSQKIMKLHL*GRGVV AHACNPGTLGG*GEWMA*AQEFNTGLSN TAKPYLDF
12762	26663	A	12891	368	50	KGRQSGVSSFPVGTVTNLTVAHNRY LFPHPGCGQTSEVKVLA\GCSLLKASRG EGFFPLPGSGGSKCPLAYGCITPISASS CDLLWVCFSSYLAY*DTCHWI
12763	26664	A	12892	227	456	KLTTLLKLF EK\IEDRTLKSKSFYEVST *IPSSSSSSSSP\ISLNTDAKKINKIP RNRIQQCIKKIIFHKSTGIYS
12764	26665	A	12893	461	89	IYQNLRSRKP DNICKW\*RCTEIQTLIHC W*QCKIMQLLWKIIWQFL*/ELNTEVPY DSIPLLDY/PKKTEC/YTSTQTLLIYCM NPIEYYS AIKRDKVLHATTWMNLENI/ ISKRRQSKSTYCMIPLI
12765	26666	A	12894	222	185	RIVMQYLHLNLGACVCVCVFVCD/CVCL CV*MCVHIHIYISTHTYIHIYVCM*ICR LS**CEFYS
12766	26667	A	12895	186	166	IFFFFFEMGSHSVTQARVQWHNHSKQH PPP\GASDPPTSAY*VAKINIFFFF
12767	26668	A	12896	55	485	TCWDCRDEPPRPALESVFLTSFLEDFES IEIADLVPHPTPCSHPIQPP**VIYFC S\KPLVTGSSSPPRKPPPSLHEPKSASL *PPSSTIQPVRSSPKG*PSPPLA*VQFP KGMTIPTLCLSPVLPVPSTIPLPNVSKP LFFY
12768	26669	A	12897	923	312	VDVIRKVQIEITLRCHLIHVRIAIKKT RANKCW*GCGEGALVHC*WEC/NYILV QPLWKT VWRFLSKLKI ELPYDPAIPLLG ISPKGNEII/CCTPKFIAAQFTIVKIQT QPRCSSMGKWKI KL/W/HIERSIDR*LE YLAFAKKKAVLSFAKTWIDLEDIMLNEI SQTQKEKYCVISLICIGIKKKKVYIEIE NKTIVITKVRIRWRK
12769	26670	A	12898	320	3	ESWRWGRIVRPHSVPGETWLCVPVPPGPP NAPDGSFPLAICPVPPSCRSI/CPP/DD CLASAGV*GGFPLPRTEASPHHSWACPQ EQPWPPQCKLKV GAPNSTALSEGS
12770	26671	A	12899	138	447	IFVFHYKTQNIYNEDTLHVIIINLWCYP GSYIKSTGRLRPEVERGLGPTTMC*FS SIKNIFYF*KLKSYRKL/WLGTVAHAYN PSTLGG*GRWIT*GQKFNRD
12771	26672	A	12900	279	1	INQSIHNNIKSTYISQCKLIQP*WKI IW RFIR/NLKI ELLYVPATPPVGV*LKELK SAC*RDNCTT/M/FTAALFCIGYGSNLG NSTALIGSRVLFPP
12772	26673	A	12901	235	183	IINYGGGPPEKKKKGGKKIPLIFYKKIK KFLWPKKKKLFGGAKNPV*AHHIFTV* IDVDTRADFTSATI\IIAIPGVKVFS* LATLHGSMNK*SAAVL*ALGFI
12773	26674	A	12902	180	19	LFIYLFYLFICEIRCHFVTQAGLQW\L IIASCFSALLGSSDPPTSAS*VKGI
12774	26675	A	12903	406	949	APVPGHGFVCSF/CGENGVS LYCPGRS* TPGLKLC SCL\CLPESWDYR/R*APVPG \LGFVFHLLT*LPPFFKDYMKSLFQFLK YLIQG*CTLV*GVRYS SFIFFFFLRR SLA/SVTQAGVQWRDLGSLQSPPPGFTF FSRLSLLSSWDYRRPPPCPANFAFVFLV



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						EMGF\TVLTRMVWIS*PCDPPASASQSA GITGVSHRARPKFVLYFKDNGEPLGGVI, HRSHIAVHWM
12775	26676	A	12904	265	385	GNGSPSLRWIGVLRGRSPTELELRH*PIF LTAASRRSLDRVSVPMWGTFLEPLSIE GLVSRYLTTNNLMERIPILYRN/PFNNET M/PESLCYRVLIIFLSKGYPRVKGRDTC YSPVRRSPAKKASFLPDAPRLACVKPVA SVHPEPGSNRTRG
12776	26677	A	12905	363	137	APGMQA*WCM/HCIPGAQAEAEAGWTEP RSSRLWCTVIMPSSHCTPAWATW
12777	26678	A	12906	315	565	TPVDHGWLECSGAIMAHC SLKFLGSRDP PASASRVAGTTGVCHHSQILFLFFVGTR SNFVAQAGIELLG\*VILLPQSPKVLGL
12778	26679	A	12907	376	412	DAWPTWRNL*FGVYVMTDR*EPRQMLTY LTA\PLKYFKSGVMAHSCN\ PSTLGGQG RWIT*GQEFET\LANMEKPCLY
12779	26680	A	12908	215	2	NIHINGQKLEF/WLGVAHTYNISTLGG RGGKIS*TOEFETSLANTVRPHLHKQK IALPLPLPLPLPTVR
12780	26681	A	12909	307	379	KR*KQPQYPLTEEWINKMRHV\LQYYSI LKKKEIL
12781	26682	A	12910	279	123	KMILSWARWLMSIIPAAWEAEAGGSVEL RS*\LRLE*AMTVPLRHFTPAWARE
12782	26683	A	12911	1	194	AKQHIIPLLARLECI/GLFTNTVTAHCSL ELLASSHPPASAS*VARMTECVHRAWLE WIFYLCVIL
12783	26684	A	12912	206	388	IELSKQGPVYKQWYVRTTPPYFPFFFFFF ETGSCSVT\RLCS/GTITAHCSLNLDP LSYSPTAAS*VAW
12784	26685	A	12913	238	426	TPLLPSQQWLKKESLWLGRVVHACNPST LKG*GGRDS\RGQ*FETSLGNIARPLI REKFLKI
12785	26686	A	12914	115	1436	AKDRHFTEV*IANKQMKRCSTSLGMREM QSKIVRYHLSE*/R*LFFFNCGNCWQG/ CKK/IQDLIHCWECKMVQPLWNIW\RF L*NHTCICHASGIALLSIYPREMKTCVH TKTCIRMFIAALFVMVETWRQPIYPSLG G
12786	26687	A	12915	282	21	IKFPPCPSTWGTTKKLFPKKKKEVMKML CFHFNLLVQNI*YRLGNEISDKAG\PV AHAWNPSNLGS*GELIT*GQEFDTSLAT IVKL
12787	26688	A	12916	254	150	TLPGRSSDFSLPEV/YLKKNH/WLGVV AHSCNPSTLGGKGGWIT*GPPHMLKVSF LPTDPTSRVKQLYNWVPHSTVLIALFPT KNPG
12788	26689	A	12917	181	24	AQWCDGIPVSKGNL/WLGMVAHACNLST LGGPGRWIT*GQEFETSLANEFHRTD
12789	26690	A	12918	75	298	LFILFTS*VD*MRPTHKENNL/LAQST NPNVHLIQ/KHPRHSQNRVWPNVWAPH G\QSSCHIKMTIMARPSGSQL
12790	26691	A	12919	251	9	KFMFLARCGGSR*SQLSGRPRRADHLR PGVQNPQGHSESQYLPKSTNFCRVWWC TPVVPATREAEA\GESTEPGRQLQ
12791	26692	A	12920	198	211	RFCFVSGDEREGKRA/RENRRETERKKQ TEDTETQREERDRDRK\ERETDTERER PREERHTEREKK*KAAFFPQTLGCRAQD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12792	26693	A	12921	438	127	FPKQLFPSRGWGVGPMTVLL RVVMERIFVRPHIKDSMWVVRSTLLGRG DALNDLFLYCWEKEDPRYKERP\RE ERERERERDRCEWK*APGWRERPVQSLR ACHPPWHRFALAGPVPSAQ
12793	26694	A	12922	158	460	EARVELLLSSRCCKPRAVITAETQPAVYR LQLEIENFPLSPRLECSGAITAHCSLD LLG*SDPPNSASR\AGTGMCHAQIVNS CKADWLVLSSRGLTHR
12794	26695	A	12923	33	484	GIQAACIPGLRLSPADAHCHRHTPSPP PSSTAPRDDVGPMQITPDNFPQDPPL\ TPFSQSLLPHRAP*PQGSSVDLPGLLFK LPQMPQTPGPPEVDTCVQIHKTSKARED VQMRKTPMAREGRHRAHRWIGALGKAP QSQRRLRHTVG
12795	26696	A	12924	335	332	RIKVYVRGHAK*LRPGP/VAHTCNCHT LGGQGMRI TQAQEFETSLGDIGRPHLYK KKKKKGGPF
12796	26697	A	12925	302	407	AQWLMAIIPAPWEAEAGLLEPRS*\AW VTW
12797	26698	A	12926	766	244	RVPRLPPLPAL*LEFSPSGLRLARSHSFQ LRSSPPPVSPST/PFSPHRSPPLSLLS LSVPS/PPLHHSFFSQRAPIHPPPLI FPSSPPAPPPPPSSSSPSSSSPPPP /PPINWGTPRFFPPPPFKNPPEINFGG PKKKKIFSPRA*KFVFLKGPPPPFFFF FFFFLGINLL
12798	26699	A	12927	127	720	WCGLLESTELQLQSLPLGYVSVIFGKIF YISGLGICCTKIFPSALPSAQAASLPL PARSALGIVFFLHFC*IE/CNYKKLP HHI*LIKTFSYGLT*LFFFFFFKTKSLIF SPRLNCRGPFVLN*NLCLRG*GNSPA*P FGGAGIEGAPHKAGLIFGGGGGAFLKKT G\LHHVAPGGASNSGTGNISHPPLNPPK GAGE
12799	26700	A	12928	308	49	KEHW*AVGHFNICVTGGP*GERKKGTER VFKEIITPNFPNLIQTIKPKTQETQHTP SRRTKI/TPRYIIKFLKTSNKEKILT TAR
12800	26701	A	12929	375	2	GCMLSLKTINILEVLANVLAQKKIKRRK LND\EQADTTFTI*FCVRQTKKSTDKL VKLI/ERFYKVATYMINFLKKSNSFHTP ATINC*KQIPFIMATKTIKYLRINPRKK CVRFGKKLTFPER
12801	26702	A	12930	202	379	SSENFSGKTVNLCCGLRLHRMISWLHTV AHACNPIT\GWIT*GQEFETSLADMVKP CLY
12802	26703	A	12931	209	376	TVGEKMYLKVKRI\WLGVAHASNPNTL GGQGGWIT*PQEFETSLGNMAKPHLYKK
12803	26704	A	12932	280	31	ISCKVTKKVTLFELKYIWNKFYIERVS IVGTTEAACEVTSNVITGPGAHAACN PST/RGRWIT*GRELKTSPANIAKPRLY
12804	26705	A	12933	1	189	QMYTESEP*CKLWTLGDYV*M*FIS*/ IQCTTQAGNVNIRE/RLCMCSGGEYMRN LCAFLSILL
12805	26706	A	12934	108	409	HHSHLLKLPNVWFSFCHFIVTVFLSL*R VFFVFY*IFLSSSHFLFSFCFCPIFMIM FPFKFILSCNIVFI*NIIFFLF/VHV*G

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						*STLVSLFVFFFLQF
12806	26707	A	12935	225	11	ILLCMEPSFLFWGFCFVKTGSHYIAQ VEVLWLFSGMIKVHCSL/KLLHSSNPPT SAS*VAGNTGSSYCTW
12807	26708	A	12936	74	12	GTHASAGVINILVFILSVFFLTHSLCI HISKYMFVYICVCICTRDFYTEFKSFC TFCFFGSSFFLEKKFPLVAGLEEQKGD LG*LKPPPPRLKKFSCLTLP/ABE*RT NG
12808	26709	A	12937	166	311	PHS*WECQMVRAPELENWQFLTCKFIRGL PL\DAALPLHM/CHRKSTQLFIALLI VAKKCNHHKKNL*ANEWINKM*YIHTTDY PLAIKQNEILIHATTWNVVTL
12809	26710	A	12938	51	296	LCMYTLHTLYMHTCIYAYICYTCKYIHR Y/LHT*IPEDANSVKHKYTHTHIVHTL VYPHTTYLMCSYIYSWVCVCVCVYIYT
12810	26711	A	12939	426	28	KGFNLVNPVFPSPRF*TPAPVFYFCGP IKKIFFFKAGGVKFDLSKRAPLFFFFLK TGSCFVP\RVECNIGIITAHCNLCPRSN DPPPSDLQVTGVKPPP\AKLFFFLW*M GFHHILDYQGETCLSQQLGWR
12811	26712	A	12940	11	213	ATAFGLFSFFETGFCSDQAGVQ*HDHG SLQP*PP\GSSDPPALASQSARITGVSH CKGPEHTSLLT
12812	26713	A	12941	416	38	WLNNHSRLGFPNCWDYICKLPRLGPDVA SLLIHNSS\GTWYGATKLESNWYFSIPI YKDHQK*FAFTWQQQYTFVLPQDYVS SAL*HNTVHRDLHDLDNPQNTLVHYS DTMLLDLMSRKYQAL
12813	26714	A	12942	361	74	IITHPSFSVSSRNHKNAYPAALGGYSVY GVAILLFHYFINKLAFTLHCGL/LNSF LR*IQEPPLG\SGSGPFCNVFLAPTEG TIVQKPDPMATFG
12814	26715	A	12943	125	401	SSFEPGRGIPLNPEVAMQKESVNILCSPR SQEFLESRIKIKVLTDLTQDEL*GQAQ* LTPPIPS\IWEAKAGGFLEPRSLRLRSC HCTPAWVTE
12815	26716	A	12944	92	306	KRTTNSPWGCSAY/GVAILLFL*IL/KL LAFTLLHGLPSNSFLRKIQEPSLG\SGS GPIFGNKLVAFGGLMIVVS
12816	26717	A	12945	322	24	NFKKNINLNPFLRGYFLFLKGGFGLTFK KVGEPLKKKKKLNQQFSYFLSTYTVK* NN*/WLGAVARTYNPSTLGGRGGWIT*G QEFGTSLANMVKKILAK
12817	26718	A	12946	2	448	GGAPMKRHGSLDRNYRVDTTTPRSQFLF QLYHNYLKFAYEATKEYMHRKETLCLPC PAIQFSFPKSNLCYRGYLCMRTCAHTQM *MYRYITYVYMHYICM/YRAICTYTYT FE*KYILQKCILLCIFLFFLQYLYVSY LNRHHFLIAA
12818	26719	A	12947	155	415	LLETGGNAGCSSWMHVLLGKIHRYGMS RPISLMAG*\GPPWLRVAGLRGRPATL GLRYGPDYSGRQQW\EYCTMGASLMQRR RVRD
12819	26720	A	12948	247	250	KYVYKYIHIVYKCVYIFTHVYGYTYLYT DVYKYTYLYTDV*ICICIYKCIYLYWYI YIHLGINMYIYIHLGINMYIHIHV*YIYI HIYI\HVIYFIYIFLYTVYK*IHIEVC

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						EYIYTLWLK
12820	26721	A	12949	25	407	EALSLLLLVLVWGLLLGIARKMYQOMNLVQYCLLVLP*P*NL*EQKRFEREVLGDRHEP*FHVLCCTHSEKSFRRFSW*EL*IRKLTVA\GGVAHTYNPNTLGHRRIT*GQEFETSLGNVVRPLFL
12821	26722	A	12950	370	106	ILYLETLKSFISIRSFSAVDSHFEKSSTVGKMLPNSITCTDPI\FNKKKSQMLMWQSSLLPFSQKLPQSPQPVSQPPSPRQGSIPATR*QLA*GSVQVMLFGSILPTVELFSKWESTAEKLLILINDFSKVSRYKIYV
12822	26723	A	12951	280	319	DQPGQHGTFL*VSH*KKKKGWM/PGVYAYNPRFLGGRGGWIT*GQGFETSLANMGKPCFY
12823	26724	A	12952	337	113	IQLAISLLGICPRDLNLTVTCS\SDTCTQMFLSVLLMVAKR*KQPKYLQIDEWINKMQCIHMESYLVSKGRKYLCKL
12824	26725	A	12953	9	186	DPTVCCQLQDTHFTYKDTNKLKVMGWTKY/CHANGNQKRAGVVIQIEYP*SKSLKSEIVQN
12825	26726	A	12954	46	381	NENTYSYKNTQMFIAALFVVTPNWKQPTCPS/SGEWINKLL\YHLMVYSAVKTN/ILVYVATSVNLRILILGKQPDKKRVLTV*PHLYRKYKLISDRKQIHGRLEVENKGK
12826	26727	A	12955	19	250	CSDMVLKACIKKLMYSYKMGHIQAMDYYTAL/NKEL/LMYATI*ANLEDIMLSKIRQTQKDNCLMVDCIYIRYAEQSSL
12827	26728	A	12956	173	163	GAKHSASGTGWIRKDFTRPGAVAHACNPSTLGG*GGWLSRSEFETSLTNMVKL/CLYKSICCTRCLLGCFFPQALSKAID
12828	26729	A	12957	301	79	EKDNQPLLTNRNVLHAIKESENHRITELKVTLRPDAVAHTCNPSTLGGRSW/WIA*GQEFELSLAKKVKPCLY
12829	26730	A	12958	314	126	KHHHFKKHNFRLCVCVCVCVCVCYKHFYLFSLSFSQ*P/CICC*CVCCSFLCCF*SATYLKII
12830	26731	A	12959	529	1697	VPFMGHISNFFSPFLRQKYLALLPRLGVQWQ*SRAHCNLRFPG\SSNSHASASRVAGITGACHHGWLFLVETWPHHVG\QAGLKT*PQV\SACFSLPKCCDRRCEPLCPATSSILNL*TMDRL/PGEPKNQ*NLLVSFMCVFPYREGQQHVYFQRLWCKREFIVRSPWAINLEKGGRLMGAV*IRIMLNLTLT*GFCTEKTVNSRVNQKLTPT*LGDE*DVKREKNINDEIKLLTCNSRYTKSYRLGR*IKLGAFCFPM\VPMGQTGRNGQLKVQV*TGTVAHVCNPSTLGG*DRRITRVQEFETNLGDHSESSLQKIKLARHGAARL*SLSL*VSWDYRCSPWP\SNFCIFK\RDGVSPYWPKA/WS*TPDLQSAHFSPLKVLG
12831	26732	A	12960	1	395	GTREFRILSEKFKKEIDFFFFFKQSSPPGPKKQTL/C*KQTTPTKPKQKTNLGPCKFGGQPKPKPKISHPQIGPPKKKNYP*GQPVWNPPGEKKEGPTPPKFKDPGANLKVMGLKGGVKKRGGKTFPQRA
12832	26733	A	12961	90	436	LWRLTSPKSAGWAGNLETQEEMLQFKS

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						EGHR/PAESPLA*SSVLSLSTDWMRPIL/MEGDLLYSKPIHFNVKISSKNTYRN IWNVWPHV*TL*PSQSD/CLK*TITPILVLLTCTH
12833	26734	A	12962	415	463	LRAKDQVLPKILVC*TLFFCAQIKKKK K/WPGAVAHAYNPSTLEGGGWIT*GQE FKTS LGNMVKPSGIPPHWI
12834	26735	A	12963	774	316	SISPTCSGKIGGKLNHRHFSKEDKTG\RY MNKCFISLVISECYLKP*EDTH*TP\LR MAKIKRADH/DKC*QRYKMTGTLIQC*R ERKMVQPLWKT*QFLKRLNIHLPPDSI PLLG\IY*RKMKACVHTNTI IWMPIASL LVKAK\AKQPKPCSTR
12835	26736	A	12964	44	395	MYFTLVWGSIGPKFLGGHQPLQGQGPFL HFLKAL**FFFPQTPGNGGGTTPAKTFP PFPTPLSSSSPCPSPAEGGSREPSLSTP /SCLHLYIGGAASNPPSPPLPPPQCSG LGYPVC
12836	26737	A	12965	424	50	MAFPFLSCAPDAINNNNKKCCRETNNEE PPNEPLKWRHIMIFFFEASHSFAR\LE CSDAISAHCKLCLPGSRHSPASAYRCPP RHLANFSAFLVQTGPPRVSQDGKDLQTS *SALLMPPLDPAIP
12837	26738	A	12966	245	44	QSKELGNYPLPSPSPSPSPAFHGLPPP SSPSPAFHGLPLLP\SWTVQPQ*RLTAT SLEDPASPSPRG
12838	26739	A	12967	205	30	QEGASLSRIKRGPGVGAWLGMVAHACNP STLGGQG/SWIT*AQEFETSLGNPHLYQ KYKN
12839	26740	A	12968	114	465	DEVSNPETTKPEPPPKKTES*P/EPKSL LWLPS\P*NSS*CANREQPPSPQPHLP HPLPTSLQVHRLP**SLPPNLFPTLYD /SPEPSLLPVIQFPA*TSPP*PPVYSSP PSPTCPLH
12840	26741	A	12969	1618	1038	VHMVQDKDINLNNQFLSGTMLLFFKETS HR*DRGPGDF*SCLYSAPIPTQPLLF*Y LPQNFIEG*PS*NSRIKGTSLKTYISRV PSFFFSFL*DGVS\TVQAGVQWHDLGS LQPPPPGFKRFSCLSLSSWDYRHPFLC PANFLDF**RRGFTMLARLVNS*PCDL PASASQIAGITRMSHHTLPHVFPPLNV
12841	26742	A	12970	197	411	EQALRSTVCYCLNPLPPAPLRPRQDC\G PCRFRWMPGGRTRWLAPVIPTL*BAEAQ VWLEARSLRQAWATW
12842	26743	A	12971	616	777	MGIHGVRHNAQLNFVFFVEDGGEWQLTC TGAGDSSWVLGEP*VFAC/PKNVLFYLH P*LFG*I*IYQLKITE*NYEGMVP/FVF RFLFETRSLSPQLECSGTITTHCSLEL VGSINSSISAS*LDGNT\GVRHNAQLNF VFFVEDGGEWQLTCTGAGDSSWVLGEPL RYKYKERLIKWYL
12843	26744	A	12972	222	389	VITEALGSDELEGRQLWW*IKIHSQVQW LIPVIPAL/LEAKAGGLLEAKTSRPAWE T
12844	26745	A	12973	425	145	QIIFFLFQKIKNQFNKASFFKKMTLEQM TSRQKNSAQISVFKKNSKWITDLNVTH *TIQLTGKN\NIGKNLQDQGLGKEILNL TLKAQSTKG

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12845	26746	A	12974	322	411	NNKKTFMSTS*KFFYCFIVQLIFETILS VRVLESIIILINYL*YCIICIFPFLFL*T *EIRKVTKFTSFPQIEEK*KCRR/WLGT VAHTYNPSTLGG*GGRIA*AHEFETSLG NTGRLPSVQKIL
12846	26747	A	12975	428	1	SRKSSSQFRLSFFPSHFLDLGAKGAVSQ DRAIALQPPGPRSR*S*RPPSRPRCFRR PRPSRSRSNKERAGEKRRPRRSLQPRPP HIAGP/VPRRQGSPSAGEAPLATDEPP PQRRSGIRGGSANIRSKQTSSLRPRVRG RVG
12847	26748	A	12976	60	294	NHCTETVLFQ*LTCVCVCVCVCVCVCT ERI/CFFKFLIGKGTGYCIYLWPKTFIL IPYIYLYSPRGRSILKKKFFFLT
12848	26749	A	12977	6	341	DSLTLPLGLECSGAISACSLCLSG/FK QFSCFSLPSSWGFTG/VPPRMPQLIFPY FSVKTGFH\HVG*AGLKLILPPASAPK CWDYRREPPRPGLWNF*PTGFKLRFPQ FPL
12849	26750	A	12978	296	42	SQFASLGFKSVLDLPLLAFCPLGKITLTL WDFSFIYYIKQE*WPRAGIFMPY\NPST LGGRGGRIS*AQEFKTSLGNIIVKPHYLV K
12850	26751	A	12979	20	373	KLYGGIWGFFFFRRGLNSATQAEMQGHN LG*LKSPPPG\*RNFPASASGEPGTTGS HHKAGIVFYIKKKPGLKTFTLGKPTPPP SFRHHWQPAPMGVYSEILGEKSLTNGWD PQTKKG
12851	26752	A	12980	380	96	PVFPWPWRAQKGSIGREIRPPRGNQK PGPP*KKKKNYPGGGGGPPSPFPPEG\* PKKWHNPGGGTTP*TEFPWPSTRGGEK KPPSKKKKKEK
12852	26753	A	12981	331	71	ELLIYSWVWCTPVVPATW*GRELVGRI T\KSRRLRLQ*AKIVPLHSSLGDRVRPC PPPPTKKLANLCPWTEGSLSFSYLLEQ FHSC
12853	26754	A	12982	383	189	RRALKSCAHSTPAGPKNAALSQAQWLTP VIPTL*EAEAGGSLELRSPRL*AMIEP \CTPAWVTE
12854	26755	A	12983	144	6	ILAQ*KTWLSVVAHTL*S/TLGGQDGR TGAQEFKTSLGNTRRPCLYK
12855	26756	A	12984	341	509	ETLYTME*YTAIEKNEIMSFAGTWLELE A\VIL\SNLV*EQKTKMLPCSPLMGWEL K
12856	26757	A	12985	387	125	DLFPPTPKLEPRTCSVAQVEVWCL/GSL QPQPPGP\SDPPA*AS*TAGTTGRHHA *EMFPF*VYFVQTSEHILGINPPGRHTK VAWEV
12857	26758	A	12986	151	350	GRGGF*PLP*IFPPGQERPGFTPPKAPP PLGFFFPG/RFFFFLRRSLALSPRKWRD LGPLQPPPPPTPGY
12858	26759	A	12987	251	1	RMSLLEKRRSNN*EARV/CGRVIYVATE VIKIMIGISMVAHAYNPSTLGGQGRRIA SAQEFETSLGNMTNPCIYKKYTHKKSRA
12859	26760	A	12988	320	3	TPWGVKDFSPPPPPGEGVFPPGRAPPPR* KFFGNFWKKRGFPNWWVRGVLFKFWG\KNF FPPNLPKSLGLRFKPPGPP*KAPPPFPL FFFFFEMEFLRCCPGWSAVAQS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12860	26761	A	12989	353	183	EYGTHTLTAAIFSI AKRWahr*GSLTDE WVRKNSSLQSM EYY\SAIKKNEVLLHAA P
12861	26762	A	12990	377	2	LSIILINFRFSLQRGKYPGPPPKKNP PQKTPPRAPKKKKPFFFFFFSFKKNF PFFFKGQSKGGFGPP*PLIFRFK\NPP PPPQKIGFKAWVFSTPPPIWGF FFFFLRWSLALLPRLEC
12862	26763	A	12991	134	298	PPNSYCDGSITLIPKSDKNITRKEKYL/ P/IYLMTIDAKVFKNVLPNRIQQ*IKRI I
12863	26764	A	12992	892	171	QT*SH/SLSRLEYSDTIIAHCSLKL MGS SDPPASASQVAKPTGHCTTMPQPHTEGF
12864	26765	A	12993	269	2	GLWCFVKQLKLTETCPHFVAPQFP LGIS KIPISILFFKKLLL/WPGTVAHTCNPST LGGRGGWTT*QGEFGLMFHHWPSKFHHG QHGET
12865	26766	A	12994	324	4	SLYPLLFQAEIYFLVTIHRSSMESCIYF FSVVPLDSLVIHQIHKI/HIKGIGML*V N*QNCFKINISE*L*YIWPSTVADTLGC QGEITRAQGFKTSLSNMTKPHLY
12866	26767	A	12995	106	531	WLLNLFAFLNDKGFVPMNRSRIFSQQK VKQRSFEGCSSFNDVGS CYVTQAGEQWL FTGVIGTL*PGTPG\SSDPPASASQAAG TTGS*HHIQLNLILYSSG*QTI*LL*TT DSTHLIFASLYAKEQLITFYFQATSLQP CT
12867	26768	A	12996	1	367	NTEPFLNIFFKDKVS/CSTIAQGQWRL YSRCSLKLGGSSNSPTSASLVAGSKGRH HYTRL*LFFYVSRPQDYLWSPVFFFSF FLSFFFWKGSFFLPPSWKARAPIWVNGS LPPRVKPIFLA
12868	26769	A	12997	3	379	YRPSSETKAVLVFFSFFSFFFLGTPGG KGP PKGAPNPTLTWRGKENFFI*KKKKP /RLI*KKGPPPKMGFKRERFWLKP KGP QFGKGEKG/SPNYPHPRGDPKAPSLWKK PQFPGGGGGGAPKKAS
12869	26770	A	12998	230	409	SCRPKLLAFLKSSTEISQRWKQPIYI/ PSTDE*INKMWHIHTMEYYSALKRTKVL IHATT
12870	26771	A	12999	310	343	DPVCTII*ICDIINL*IECSKVW*SLKF YKILILFNVCVWPSVGNCHKWLCDCVV* KQW/LWPGMVAHTCNPSTVRGGGRIV* GQEFETSLGNIVRPSLYNNKSCI
12871	26772	A	13000	390	289	IKLCQPRGVKLDSEFKRAPFFFFFETRS CFVS*AGVQWCN/LGSLQPQTS GPNPNTSA*LSLIFMCSNSYVCIVK
12872	26773	A	13001	1	289	GILRQISVNYLPVGRSLAQAGVQRCDLG SL*PLPPKVKQFSCVAGTTRGCHHAWLI FIFSRG\GHPVKGASSDSPTFGFSKAG ITRLSPRALACT
12873	26774	A	13002	359	105	KQKKNPSPPPGGGGGQKPG/PKPFPPN SRDFPPKNQSPFFPKLKKKFFNFY*KAK NP*KPNPPLKKGKPKGFFSPPPLKKP PNV
12874	26775	A	13003	243	293	MNSQFLKRL\RIESPYGSVISLLGTYST EK*KACPCKTCTQMFTSALYIIAKKW\N KCPSTVRW/IKLWHINTMEFFCQ*KKFH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CIDMPQFVHLTVEGHLSPFCYYI
12875	26776	A	13004	465	307	SEACFILKLFMFCG*CCLFVC\SILLVF YFVFCFVLFCAYYMQFFNQCLFG
12876	26777	A	13005	207	3	DGSLTMLPKLEC/RWLF TGVIMAHCHLE /RLGSNDPPASASRVAGTTGVCHHA*LI FIFFVKMRSHYPTRP
12877	26778	A	13006	2	56	DLALLFRL*CNGMITAHCNLK/RPG*LL GSRDPPTMVS*STGITGMSHEHRPSPS CDF*RSCSVVQAVVQVHWDYSSL
12878	26779	A	13007	402	74	FGASLLKRHFLFFLSKPLVYNKKIPRPL VFLKKT\PPPPGRATPFYCCFFHKEGP GFGVKKEG*PKG/SPPPPQRGSTPPFFL GAFKKPKVTPFFKKNPCKTLKGPPFF
12879	26780	A	13008	356	145	RPPPPFFFFFETVSHPVAHAGVQVHDS LQL*TP\SSREPPASAS*VAGTTGVHYL PGSQLPILEHSRR
12880	26781	A	13009	227	353	GWSELT*/SN*AQWLTVPILAL*EAEAG GSSEPRSLRS AWATW
12881	26782	A	13010	249	32	NPD SHSWAWWCASVVPQTQKARVGSSE SRSLRLR*AMIVP\CTPAWVAQEPLSLK KPPTIETLFPSQDPSQ
12882	26783	A	13011	247	403	TPGGGGKYFFFWGPPQKKNRGGGFKNGGG GKTRGPP*KQPASSSPFAPPPFFWGAPG FSPPPRF\KPPPPVFFLGPPKKKIFPPP PGGLFFFLLGGPPSPFFFFFLLGGGPL FFPGLGAMGPMAGFRSLAPPGNSLSKKK KSEGLGEGGNSVLTRVLLISSYQIPGNP R
12883	26784	A	13012	206	386	TREAQTFWFPLYS*KAL/WLGTVAHT*N PSTLGGQGRITSSQSESETSLANMVKPH LLEI
12884	26785	A	13013	354	31	YKMNIWDI IHI*HT\YIPVVPKGKERKR KKLEEYL/QDIMTKNLFNLMKNMNIYFQ EVQQTPSRINSQTSTPRHII I KLSKYKT GREQWILSVMLALWEAEVVGPPPEVRS
12885	26786	A	13014	1	419	EETSF GKARCLPGYPGFHRRRLRSRPL LS*MPLSHPPQGPSQPPAGSMSSSPATT STCSCSPPAAGCTRGRTTGRPFWTASGP AELD WASGSSV/EALTSGLPARGLWGQY AGLGVP PRL LGPMTSCCMSLPFPSPARP
12886	26787	A	13015	109	426	TSLGNIARPH*QTHMATIRSVPPPSWKD ST*LR LHPPPHMCF/PD*SLKSN*Y*H YLVNP\IWPM LTL LFVCLFVCFDRVSL CCPGWSAVVPSRLTAAS TLWVQVILPP\ RLAN*IFFLRWGLAML PRLV*NSWAGDI LPP*PPKVLGLQA
12887	26788	A	13016	149	422	LKRIFFLKVVFTHDTAPGD PDNMCPYSC F*NQI I KSGLFFFKKPHL/WLGE GAYPC NPTLLGGQGRIT*FQBFETTPANMAKP LLYKKYKN
12888	26789	A	13018	162	377	QSPGYPERVSKLPTITQRGMWMMHQP SFV CTSL*NV*TGWAQWLTVPVPAF*ED\AL AGGLLEVKNLRPAWST
12889	26790	A	13019	205	427	IQTGGPPARPFLWPWAPGKK*RVPPGGG PPKKKKKT PPPHPGGEREGS/PFSKKKK KKTPKKRAGVFFPGGPRPKEGPGWGP LD SKFVGAPPEPGR LGNGPGKI FFGPGP FFPLQPQKGRP*PGGEGGSFFF LGLVPP



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12890	26791	A	13020	248	358	LGEPSIFCLDLPENA SRCGGEAQWLLPV/I/PAF*EAEAGGSF EPKSLRPAAWAT
12891	26792	A	13021	2	434	ITEAGSDTQEIHTHTLYTHLCVYWRFFTK KAQVKKKVWWHM*PQLLGRLEMGGSLP RSLRLQGAMTLPVTSTT\QAWAT
12892	26793	A	13022	162	410	LTQKTAASQIILSFSSTSLKIPISSES GGGGSVSVTQAAEQWRYHSLLOP*TPGD KRSSHLLGIPHP\SSWDYRISKDWVMPV
12893	26794	A	13023	250	40	LIKLNIFSCSLAIWTSSCMTSLFKYFAH FSFF*IDFYSSYYILDTPNPFRRN/GITN ILSSSVTCSFILFVV
12894	26795	A	13025	264	1	VSSTKHGKLRLEPEY*CFIHH*EEKVFE SYFEY/PCQTFILRKETVRGAVAYACNP STLGGQCRWII*EQEFETSLTCIAAALR VTLR
12895	26796	A	13026	110	523	CIDSSSWTQTDCKEDRLCPGTTGTGTCAP GLLFLSAPPLGPF*PSQAHPSFHVSLSG PSPGLRPQLDIPHPSTSIAPRPLPGPA S\LPRLPEHPSLPSPGTGACPFLLPCLGE QRHWPLPTSLWLGLDGHCLATPSVS
12896	26797	A	13027	52	53	CPTLLQLTLC/LPPQASAMVDAPP*ARP LPPSSILACCTSGEQGSVVVGLAEPVKG YNLLVCRLLRPLEKCGIWWAVSRFSLYS LSWLPLARKG\NPLTACASWVR
12897	26798	A	13028	262	381	HFGRLRQVDRSLSPGVRDSLCKNVKP*QI IYTF*FSVSLSVINTYLGKGPSTVAHTYN PSTSGG*GKWIA*AQEF/TSLCNVKP CLY
12898	26799	A	13030	1	846	FRPIQAGRAPWALTLP CMGFTGEGSPALL SHSSRCDIQMGCNTHAVDDSTGEGPFHK GRMRESCWLRTPRCGLYTKGVGGPGMEG RERRSRSRQHMPGRGHSTMASWSLRQC MRLKLQWASDILLSQLEMQIPSLPPGESG SLGLTGPRSLH/CEQTIGLSPTPGESWS EELG\GGIVGGGRGTVAGRGGHREAGNK PSGTWGRQCCASGDKAMSI*LTSLY\AR RGEPPGPRPVRKWLRESSQNRI GGEGR WE*GQRRSREGRECPVGWGRKKPLRWG LMWS
12899	26800	A	13032	308	1	KHYHDFWCWIIILALSDAQSLDHTCV\CV CVCVCVCVCVLRDQGSLSCL*CEG*LVP HFVPGPVLCLLSPVIYVCFICSLTCKVE SLSNFFKKLNKALLRHCI
12900	26801	A	13033	763	244	FLGPRIIGLRHEISVETQDHKSAVRGNN THDNYENVEAGPPKAKGKTDKELYENTG QSNFEEHIYGNETSSDYNFQKPRPSEV PQDEDIYILPDSY*L/CQNIDFCYWMIN IHCNFS TAKTRNQT KC*STVDWIKMWWY TYTIEYYAAVKK/DTKLTWEQKI KYHIF SLKSGS
12901	26802	A	13034	326	58	EHYKCNVCQKIFQKL*/HL*SKKHVYAE DKYYKYKDGVVPLLSQIILYTFYTRGK P*SSCSNFVQNQIIYIGQKSCCKNKF GN TFFKKP
12902	26803	A	13035	199	3	RFIYNHVKCITTFPLPHFYF*KLVL/WLG TVAHAWNTSTLGG*GGRT*GQELTGL DNTARPHLHTV

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12903	26804	A	13036	94	448	GSCATSMAPKFDTRKTAVEPGVVHGI RKP LEKVCADLITGKKFKNL/KVKG PVCMP TKTLKITTRKT PCGESSKA\WDGFQMR IQK*LTNLHSPSKI VKQIISISGAPGID SEVTNADG
12904	26805	A	13038	964	1717	HKLSCVKDLKDFMRQAGE\VTFA\DAHR PK\LN EGVVEFAS YGD LKN AIEKLSGK\BINGKNINLIK GSK\RPSRSRS RSSDPGTQKSP LGP RSRSPSPVVRKP*QPVQ EARSRE PGARSQVPVPVK*GPPPCPEKEPQK \RGS LQSKILSP PSILWIRPEVSGPRSK VERSVDSGN
12905	26806	A	13039	2	725	SLLFSPVLPFLFLPLAYILQNLKPLQF SPDLKSKHLIFFCNAA*PQYKLD RSSK*PENG TLNFSILQDLNNSCRKIGK WSEVP EVQAFF\SHQSLPSLCAQCNS/CPN LPS FPP\PVPSVPTSPVTESE*SSFST DPSD LSLPPQALLIARPS*VPILPQP PLLHPI ILLSPPLLTPRPAYSFIP*L/CP PPPAQ QFTLKKVAGAKGIVKVNAPFSL SQIR*H LGSFSSNIKIQPSSWL VWQQP
12906	26807	A	13040	1131	2	DGVSLSPRLECSGTISAHCNLHLLCLN DSPASAS*VAGITGPATTPPLIFVYFF LVETGFHHVQSGLELPTD\SDEPPASD SQSVRITGVSH/AYLACSQF/CTRC*FP II*EQCVNMNINSSK*IFILISYLRWM NKDPI/VIIERLLVRMPEGQSHA AW*NK TNKQT*ILELVLVSVTSCGVS VRFNLSIP *VFPSTK*EGWMRCVNPSTLT*FI PQVA *TCQEHGLMKIQ*NPGLDPSIVSD HQT Q*EPSVKQVLDISHDKLPM SLEELYHCR HTLASGKQISGV PRTIFLNHFHGFYFIY /CIFEMESCSV/SQAG/VQWRDL SLQA RS/PGSR/RFSCLS/LPVQHP PPGPANF \CIFSGDGVSPC*PGWSQSPDLVIR
12907	26808	A	13041	97	626	ICFTQVKVLNESQVQWCMPPVVPATWEAG AGGVLEPGS*EL*/CPVNSHC PPAWAT
12908	26809	A	13042	2	431	HDPDTHSQIKVIKLMQSEFCWGWAW*LT PVIPALWEAE/AGGSPEVRSS
12909	26810	A	13043	405	1319	RYRKKLQNKPLWLH/CLLLLPNSATR*T LQK*SK*ISPLESSA**KEPPFLSVLSV TSVKT/SAIPMPPHWENVNTQVPYQLIP LHNQTHEYNEVANLFGKTM DRNRIKRIQ RIQNLDLWEFFCRKKAQLKKKRGVPQIN EQMLFHGTSSEFVEAICIHNF DWRINGI HGA VFGKGT YFARDAAYSSRFCKDDIKH GNTFQIHGVS LQQRHLFRTYKSMFLARV LIGDYINGDSKYMRPPSKDGSYV NLYDS CVDDTWNPKIFVVFDANQIYPEYLIDFH *FHFQISVVKEALFFAGRFALQSSSH
12910	26811	A	13044	23	450	RSRAAAIQLGQRLRLPGPDS PRLTGRQL EPGTGRGSR AKRGPCSI FRFRRET PQP R EGGEALGATSRQAPPPC PPRQPWELDAS AKAAAVAPPKVGFKA VSRDPRAEALGG KGSP\GGKGS LKGVAHR*GGLGPL*GAP EAI
12911	26812	A	13045	172	16	AHVSPEVDKTKFW\LG PVAHICN SSTLG GRGGQIT/R/QQEFETNL TMEKPHLY

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12912	26813	A	13046	181	9	YKNGPAMLPRLKCRAT\IGSNMAHCRLLD LPGSSDPPSSASQVAGTTGTCHLGARGG MV
12913	26814	A	13048	2	3507	YVRVSLPPPPPPAAGRPGA AVADDAREEE EEAAPPPPPPPPPRLAAARPPGSQPRPP AAGEAQAAADMNHQQQQQQKAGEQQLS EPEDMEMEAGDTDDPPRITQNPVINGNV ALSDGHNTAEEDMEDDTSWRSEATFQFT VERFSRLSESLSPPCFVRNLFPWKIMVM PRFYPDRPHQK\SVGFFLQ\CNAESDST SWSCHAQAVLKI INYRDDEKSFRRISH LFFHKENDWGF SNFMAWSEVTDPEKGF DDDKVTFEV FVQADAPHGVAWDSKKHTG YVGLKNQGATCYMNSLLQTLFFTNQLRK AVYMPTEGDDSSKSVPLALQRVFYELQ HSDKPVGTKKLTKSFGWETLDSFMQHDV QELCRVLLDNVENKMKGTCEGTIPKLF RGKMVS YIQCKEVDYRSRRREDYDIQL SIKGGKNIFESFVDYVAVEQLDGDNKYD AGEHGLQEAEGVKFLTLPPVLHLQLMR FMYDPQTDQNI KINDRFEFPEQLPLDEF LQKTDPKDPANY ILHAVLVHSGDNHGGH YVYVLNPKGDGKWKCFDDDVVSRTKKE AIEHNYGGHDDLSVRHCTNAYMLVYIR ESKLSEVLQAVTDHDI PQQLVERLQEEK RIEAQKRKERQEAHLYMQVQIVAEDQFC GHQGNM YDEEKVYTVFKVLKNSSLAE FVQSLSQTMGFPQDQIRLWPMQARSNGT KRPAMLDNEADGNKMTIELSDNENPWTI FLETVDPELAASGATLPKFDKDHVMLF LKMYDPKTRSLNYCGHIYTPISCKIRDL LPVMCDRAGFIQDTSLLIYEEVKPNLTE RIQDYDVSLDKALDELMDGDI IVFQKDD PENDNSELP TAKEYFRDLYHRVDVIFCD KTIPNDPGFVVTL SNRMNYFQVAKTVAQ RLNTDPMLLQFFKSQGYRDGPGNPLRHN YEGTLRDLLQFFKPRQPKLYYQQLKMK ITDFENRRSFKCIWLSQFREEEITLYP DKHGCVRDLLECKKAVELGEKASGKLR LLEIVSYKIIGVHQEDELLECLSPATSR TFRIEEIPLDQVDIDKENEMLVTVAHFH KEVFGTFGIPFLRIHQGEHFREVMKRI QSLLDIQEKEFEKFKFAIVMMGRHQYIN EDEYEVNLKDFEPQPGNM SHPRPWLGLD HFNKAPKRSRYTYLEKAIKIHN
12914	26815	A	13049	30	477	VRAEHCAVWERNFEETVRWTSVKFLMTS PEIASLSWGQMVKGSNTTYKDCKWPG GSRTWDWRETGTEHSPGVQPAAC\DVKE VVEKGVQTLVIGRGMSEALKVPSSTVEY LKKHGDIMRVLQTEQAVKEYNALVAQGV RVGGVFHSTC
12915	26816	A	13050	179	389	NIETIQSMFPI/DNEMKLEINLKKATWG IHKYASQVLWFMP I FPTLWEAKVGEFLE PRSSRSVWETWRDPI
12916	26817	A	13052	466	1489	PGKGEMRTRSPSP LAIVPRPQARSPLL CAVSPMASASGATAKHEQILVLDPPIDL KFKGPF TDVVTTNLKLRNPSDRKVCFKV KTTVPHRYCVRPNSGIIDPGSTVTVSVM

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						LQPFYDYPNEKSKHKFMV/QIFAPLNTS DMEAVWNEAKPHELMDSKWR/CPNENDK LNDMEPSKAVPLNASKQDGPPTQPHSAS LHDTETRKLTECKRLOGEMMKLSEENQ HLRDEGLRLRKVAYSDKPGSTSTASFRD VTSLLPSLLVIAAIFTGFLFFFWRRSL TLVAQAGVQRRDLGSLQPPSPGFKQFSH LSLPSSWDYRRPPHPANFCIFSREGVS PCWPGWS
12917	26818	A	13053	892	189	SYDPGALGCRPAPRSRGKSGGATRDMH PMSRERAKFVKSGL/YCKTTRELMHAR CCLNQKGTILGLDLQNCSEDPGNFHQ AHTTVIIDLOANPLKGDLANTRGFTQL QTLILPQHVNCPGGINAWNTITSYIDNQ ICQGQKNLCNNTGDPMECPENGSCVPDG PGLLQCVCADGFH/GIQVYAPGLVLTAY VLRDSGSHHSIRLHSA LGDPAPKSQDFM NYIGLTIDLRSI
12918	26819	A	13054	423	12	SFNQKNPLRQKCSLRPTRPASQSLATWP GQSTRFEQALPWALWDPQSKRAE/MQL EPPHAHTWTHAHTCGHTGA/FCSAHTEV YVHLSPVHAHTHAHTHSPPVHTCGCRL HAHTH/PQTPSPPGLLSLLAVARPQS
12919	26820	A	13055	16	349	RRSGKNDPWTQSPRAASHTRCPHBAV AAAAMPKRKTEGDAKGDKAKVKDESQKT S/ARMSSKSAASKAYAKPIKAPAMNGEN VPNGIQRKLEAFYDLQACRHLTRLIDFA
12920	26821	C	13056	716	594	MMQTETGVMPPQARQCLEPPGAGTGRKD SPLYPSEQSWPL*
12921	26822	A	13057	353	2	IGNPGKTTFNKPPPPKFFIESKFFMFLF FLVKTRSCYVAQAGLQTPG/SSDPSASA NQSAGITGVSHHTQSEILKYTVFCLTFQ TPEYTIPTWSIPCCSHFSCYLCLFAC FLRQSF
12922	26823	A	13058	864	529	EVSTSKTAGCRGCALVISMLCIIFFQGL FTRALLRITCSALLHADWPEISFVVVVVF FKTESCSVAQDGVQWCDLRLSKPPPP/G SSDSPASASPVAKITGMHHHARHGLKS
12923	26824	A	13059	2714	1376	GRYDGLVEQLGGRATPAVGFAMGLERLV LLVQAVNPEFKADPVVDIYLVASGADTQ SAAMALAERLRDELPGVKLMTNHGGGNF KKQFARADKWGARVAVVLGESEVANGTA VVKDLRSALAVGVILGVGALIGWRYWNS HQVDSARSASLAYQNAVTA VSEGKPSI PAAEKFAAENKNTYGALASLELAQQFVD KNELEKAAAQLQQGLADTSDENLKAVIN LRLARVQVQLKQADAALKTLT/TPIKGE GWA AIVADLRGEALLSKGDKQGLLSVTL LSGCSL FNSEEDVVKMSPLPTVENQFTP TTAWSTSDSGGIGNFYSLNHPALADNVV YAADRAGLVKALNADDGKEIWSVSLTEK DGWFSKEPALLSCRVTSVWPNNQTEKFN KQRTGPAVAEPEQAGVRRHYLYPFTGG YRRRRACQAERPAARCA TEHGSRN
12924	26825	A	13060	99	254	RNHLVAFKELSALKVKVRVDWAPWLMVPV IPAF/LEAKVGRSLEPRSSRPAAWT
12925	26826	A	13062	127	386	FSYYYYFFFLFFLCVFVIPGEPFLKMKL GPKPTIMLKEKKGGESYSELFETDQME

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						WL/TPVIPTLWEAEVGGSEHRSSR
12926	26827	A	13063	1	209	GKYILLKLVFCFLRQGLCHLAHCSRL PGSSDSRASASQVAG/ISITGVHHHARL NFVFCFFFLVCF
12927	26828	A	13064	132	1	SHAMCCNYLKRFGWARWMLPV/IPALWE AEAGRSPEVRSRSAL
12928	26829	A	13065	269	134	TLWSVFASS/WAWWLTPTVILAPWEAKAG GSPEVRSRLRICKQKVLS
12929	26830	A	13066	853	461	RLWRSVSQFLCACVHMCVPSVCVCGLAH AGTYAVSTCVH/MCVCMCARITLAKI CSETSGNLLFRKIISLLDLFTLNFSIKY KVQLVLKSRSLAWWGRIKLLTLSPFSD VNTFERINYWLINDISIIR
12930	26831	A	13067	57	2066	AQPTGRQTSTVAPTATARSRGGRVPF PCPHAPATLLSTSRVTPASPAASKAL RLSASALFCLLLINGLGAAPPGRPEAQP PPLSSEHKPEVAGDAVPGPKDGSAPFVR GARNSEPQDEGELFQGVDPRALAALLQ ALDRPASPPAPSGSQGPEEEAAEALLT ETVRSQTHSLPAAGEP/EPAAPPRPQTP ENGPEASDPSEELALASLLQELRDFSP SSAKRQETAATAETETRTHLTRVNLES PGERVWRASWGEFQARVPERAPLPPPA PSQFQARMPDSGPLPETHKFGEGVSSPK THLGEALAPLSKAYQGVAPFPKARRPE SALLGGSEAGERLLQQLAQVEAGRRQA EATRQAAAEERLADLADLLQYLLQG GARQRGLGGRGLQEAEEERESAREEEEA EQERRGGEERVGEEDEEAEEAEAEADE AERARONALLFAEEEDGEAGAEDKRSQE ETPGHRRKEAGTEEGGEEDEEEMDPQ TIDSLIELSTKLHLPADDVVSIIIEVEE KRNRRKKKAPPEPVPPRAAPATHVRSP QPPPPAPAPARDELDPWNEVLPPWDREE DEVYPPGPYHPFPNYIRPTLQPPSALR RRHYHHALPPSRHYPGREARHAQQEE AEAEERRLQEQELENYIEHVLLRRP
12931	26832	A	13068	282	53	PGFPQGKFRFKKILPQDYPFQGAPNSK ARPGQGVPPGIPA/LWRVKKGGPLRSGG PGPPGAKGGTPFLPIPTTKKS
12932	26833	A	13069	177	2	VSLCRPGWMECSGVISAHCNLRPLGSSN S/PALASRVAGITGARHHALLNSLFKVL SRA
12933	26834	A	13070	789	302	PHPEFYYSFQYFYFFISFHTRHFIVH YFISSHFISCHLASSSSSSSSSSSSSS SSPPAFHYSFHHFISFHLAIHY/HFIIIS FHLFHLFSSFHSISFRDRDLLYCPGWSV PPHPAFHYSFHH/VHVMRHFILRQTRS IAQAGIQWRDLCSLQPEVGSSRSA
12934	26835	A	13071	193	2	PPYLKSHSQVDLSPGVQDQPGQHRETPS /LTKN/TKVSWVWCTPVI PARWEVEVR ESLEPRCSTRA
12935	26836	A	13072	122	1495	LLSDFFFFETE/SRSIAQACMQWCYLSS LQSLPPGFKRFSCLSLPSSWDDRCPPPC LANYCIFSRRDVLPCWPWSRTPDLR
12936	26837	A	13073	178	347	CCLCNDNSVLLCMYLLVCMHACMHALY IKTWK/MQLGAVSHACNPSTLGGQGEWI T

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12937	26838	A	13074	165	34	FILSFPFETVSFYFVAQAGVQW\LIIAHCSLDLPRSSDSPTSAP
12938	26839	A	13075	205	105	GGWVQWFMSIIP/AIWEAKAGGLLEPRN SRPVWAT
12939	26840	A	13076	3	357	HEREYTQAEKRKFIAFFFFKMGSCSVIQ ARVQRHDLSSLQPP/RVAGTTGTHYHTW LIFVFSRTDSRLPSSPRSPLTSVISLIIPLSLIPTTYLTTPSRPSSTSPPSHPSFR APLTSDP
12940	26841	A	13077	3	477	STPALTARGLSGGSRASVAMVLESEQ FLTELTRLFQKCRITSGSVYITLKKYDGR TKPIPKKGTVEGFEPADNKCLLRATDGK KKISTVVSSEKVNKFQMAYSNLLRANMD GLKKRDKKNKTKTKAGSNSS/ATTAAP AAAATAATTAATTAATAAQ
12941	26842	A	13078	1077	1566	RQVTSLDPLKTFPRTSLEFTSPTGQLDS GATAFTVVWPSGAPTPRGRESAAHQGN/ YPVGQRS\RMAGLSPRSFCWWEVSFSR/ SHSC/ICWVQLGKSAVLEQQSRGPGAHE GSRRRGGSSPPCPPLQTQLVFSQPQLSM SAPIHRLSVTLQGDCISTGGAPSRCLRA
12942	26843	A	13079	3	396	HERGRKMVSVT\RLIQLRLNWSAGHDLO GKQLRLRYQEISKRTQPTTKLPEGPSHKL FNNYY\CTRDGRRESVPPFIIMSSHKAL VSRMPAYSFAEAATDKKAVTPAPSIYRG EQSSDHPYLRHCTLTVTRL
12943	26844	A	13080	467	109	SLVPVVSPhLKEPSCRVLIENTVMLVPKE QEFWSKEAGSLFSPVPVFCWTPSIVFS SSFFFLFRCVCFVFFFCVFFVFF\LLF FGTKKALYLLRARGCKQYKNQKLIWYLT FLSSLVK
12944	26845	A	13081	458	51	VSLFCTVAPLLLLPEGIFFSCSLLEVKA PMRDVSGVFLTLFLYSLVFFPLGVFFFL FFFLILPPPKIFFFFFCVAFVFFSPAF GAVFLF\SLWSSVLPVGVFFFTACVFFF FFFFFFFLQSFALVAQARMQWR
12945	26846	A	13082	23	327	RSDSEGGRRGHKVIPIPIYTHTYIFTI YTOIYICLHIYACLS/LICTHIFISYI HTYIYISYAHYIYLIHTHYLIHTYHT YIYIYLIHIYSSWVCKGS
12946	26847	A	13083	352	153	KKLVEYYSAIKKNSVLH/VSTMRLKN ITLSLKTQSQRHLYIIPSVRNVQNRQV HKYRSRLVDS
12947	26848	A	13084	121	417	DYDYCYCYYPKIYLTCLLYFY\VGNYIY THYVRHVYICETVMPVYTHIHTYICIY IYIWKETTWLFSCGISKTYRTHDLAYTY LVFCLTHVTFHVSST
12948	26849	A	13085	242	12	LSSRLPMLLETKEITSKILPSRKL/LPY GWCFSFKITWVSQIRNRL/AQWLTTVI PQLWEA\SGLLKPRSRRAWTTW
12949	26850	A	13086	274	340	GGEKKTGPGFLEKKSFFGGGIFGPPP/P TKGVPFPSPKFFFPKTKNFGRGGGP KIPPPKDFFSKNPPGVFFSP/YKKKK IIFPPPVLGPPKDFLKSPPPFFFFFYF FFFFFFFSSQEVNLKALSSTSEIIFFYLV
12950	26851	A	13087	241	405	PPPSKIHIHGNFRKMSDVKNATGWAWWLT PVIPARWEAEAG\VSRLRPNRPAWAA
12951	26852	A	13088	537	375	KHSLTSLRLLECRGTILAHCS/L/CTSL

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						LGSSDLSLQPQQIAGTTGACHHTHLEKIF
12952	26853	A	13089	448	186	GALVFPSSQAPPCCPPKMEQSF F F F F F F L ETGSRSVSKAGVQLHHGSLQPPPPGFER SSHFSVTTI/TYLYHHRLLALHVLFELHIN GIMHR
12953	26854	A	13090	365	191	GQEREKEREREKRRQKKREVE/REEEKE RVRDLESESNRALERERSALVDRAPLSR PG
12954	26855	A	13091	148	316	DKMESCSLAQTGVQWHD/LG/YLQPSPL GFKRFCLSLSSWDYRWETSTEPFQQAV F
12955	26856	A	13092	712	229	FVAWVKMAEYLASIFGTEKDKVNCSEFYF KIGVCRHGDRCSRLHNKPTFSQEVFTEL QEKYGEIEEMNVCDNLGDHLVGNVYVKF RREEDGERAVAELSNRWFGQAVH/GEC TRGGGFCNFMLRPI SQNLQRQLYGRGPR RRSPPRFHTGHPRERNHRVFP
12956	26857	A	13093	835	405	ELIERLGPNQKPPILMWKPMPSPSNMKA SAALLCLLLTAAAFSPQGLAQPVGINTS TTCCYRFINKKIPKQRLSEYRRTTSSH PREAVIFKTKLDK/EICADPTQKWVQDF MKHLDKKTQ\TPKLLNIHDWNLENQAMT LRKPN
12957	26858	A	13094	1137	424	LCPSHFAPTTLTQPGAHKNMCCIKSRFK RDLGLCRTCLVNKMTSSILGKSHRHSL VSINQGNALWKAAG\PLSWKAGYC\QG FSPCDSLKYG\SWDEKDLTVPQPDTHKG SVLRWISKRGKPLAVEIEGRATGLPGLA PWGTE\CLGYKTPIV\HLENSEMG\ENR PYGGEARHVCNAALLFFTPLRCLGGEK HKSGLRAHPVIVLSLELNVDIDSFAHMF FADLLLIITLLSCYIPFC
12958	26859	A	13095	1	324	ARGERERERERERERERERERERERE RERERERERERERERERERERERERE RERERP/RPRVLFFVRGREGSHPEKCB KKERAPFSRALRKISIE TRGGVSITTEA CVFVIGAHVRCSRVIYI
12959	26860	A	13096	508	840	DGVSLCRPGRTADCSGAISAHCKLRFP SRQSPGLSLPSSWDYRLKPMRPAFFFF CIEFF\VKTGFLVVSQ/AMGLDLLNS/SI PPRLGLPKCW\DYRREATAPGQELLLNR TGM
12960	26861	A	13097	53	254	WPQTASCLVAQAGVQWSDHSSSLQRQTPG \SSHPPASASQVARITGMHHCWLHLII LLRAHGSSPLC
12961	26862	A	13098	329	67	GPGAPLLKGEKLLPKPEPPRISPIVSFAF FAWGPPPGYCFLLKKGPF\VFPPSFFG KKKNSPPPHINGGAKTFPNPPLLFSSF FFF
12962	26863	A	13099	253	444	EGAFSLGTFFYFIFFLVLSNTFLLSIKNQ QIWNKKTW\PSPFLLPTLIALTTLLLP ISPFILII
12963	26864	A	13100	341	590	PMASQICIGRIPPFLYLKWFYWPQKVV HTCNPKTLGGRGALITQGGKFENSLAN\ MAKPHLY
12964	26865	A	13101	55	184	RLREPTPLYSE/HAPTKYYRMAHHNYPH SPPIQPQRHHYRVFL

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12965	26866	A	13102	433	762	RNLLNCKRGLERKGCASWPVPLFLQR RVWPRPTAELNEACMLAQHNCQNVKME YFQLSFTKRQEI/WLGVVAHACNPSTLG G\QGGGIACSQEFKTI PSSKVRPCFYLK
12966	26867	A	13103	349	250	DLFFSTKPPPPPPPPKNLGP\GPFPPP FQEG
12967	26868	A	13104	3	236	YPQHYPSCTFQYTLKTKNHNFLIFFEV GSCSVVQARVQWCHHGLQPP/NSSDPP ASAFQVAGTPGVSHRAPKQNF
12968	26869	A	13106	154	4	KKVKNTVHYNGKYFLKSQNSTFLKEIL /WLGVAHTCNPNSTLGGRSGRIT
12969	26870	A	13107	391	150	RPPKKPNKKYSQITSKGIMVYTRKYL TKKKAMSQALWY/V/HAVPATQEAEEVGG SCEPGSSRPCTMIMPMTNTHCAPAWAT
12970	26871	A	13108	90	252	KVGDGGRCLVFCFYFKRQGFVTAQAGVQ W\ATIAHCSLKLGLSSDPQNYEDSWGT
12971	26872	A	13109	197	414	LYEFIKITVLLGLGCPGRYGCNSQRF SLEMEFHTVAVARVQWHDLDLQPLPPR PNRFSCLR/YPQSSWDYR
12972	26873	A	13110	2	317	GRVGANVHKGHRQRTYGSVIPHLPLHV LKKTFSLRDFHFSVSLKK\NLVLTCLHL FL/GVTRPRNDPFVSMMLLFTAFDRPS TILGTGLLYTEGLTVALRLAYLR
12973	26874	A	13111	413	162	LILLPQPAECLQLQASATLDCGLRRC RDCRRSLVHSLVNGAQAQVQWRDLGSLQ PPPPS\TCLGLPKYRDCSLCPAATPSGK
12974	26875	A	13112	40	296	ESRLSALYIYHICVCVYNREHLLYGIHM /SIHTYTHTHTHTHIYHMRFALEDKF ICSLLCSRQDNAFILVSVKLQRKNYFLT RR
12975	26876	A	13113	2	288	FEPRCKNSARGKVPRGFSPNLPHVTET PEGSKTGFELES/RRHRQIHSSAQCP LTAVPGAGDAIPEDASGWTWPLPLHAQNC FLLYIQAPEQPPA
12976	26877	A	13114	685	340	LSPFRAGSARPTGPPTDAPQQRSTWTCG ALKPRRRALRDAENLFQELQEHFQALT ATLNLMEEMGNRIEDLQ\NVNDL\MV QAGIENSIKEQMLKTVTANMSVFGDGAS YRSH
12977	26878	A	13115	65	3021	GVLTMQMGDEKDSWKVKTLDLILQEKRR KEQEEKAEIKRLKNSDDRSKRDSLEEG ELRDHCMEITIRNSPYRREDSMEDRGEE DDSLAIKPPQMSWKEKVHHRKDEKRKE KCRHSHSAEGGKHARVKEREHERRKRH REEQDKARREWQRKREMARHESRRER DRLEQLERKRERERKREQQKEQREQKE RERRAEERRKEREAREVSAHHRMTRED YSDKVKASHWSRPPRPPRERFELGDGR KPVKEEKMEERDLSLDLQDISDSERKTS SAESSAESGSGSEEEEEEEEEEEEGS TSESEEEEEEEEEEEETGSNSEEASE QSAAEVSEEMSEDEERENENHLLVGKN LPGDRVPVPESRFRDSDGSESEAAEEV EGTPQ\SSALTEGDYVPDSLPLPIELK QELPKYLPALQGCRSVDEFQCLNRIEEG TYGVVYRAKDKKTDEIVALKRLKMEKEK EGFPITSLREINTILKAQHPNIVTVREI VVGSNMDKIYIVMNYVEHDLKSLMETMK



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						QFPLPGEVKTLMITQLLRGVKHLHDNWIL HRDLKTSNLLSHAGILKVGDFGLAREY GSPLKAYTPVVVTQWYRAPELLLGAKEY STAVDMWSVGCIFGELLTQKPLFPGNSE IDQINKVFKELGTPSEKIWPGYSELPVV KKMTFSEHPYNNLRKRFGALLSDQGFDL MNKFLTYFPGRRI SAEDGLKHEYFRETP LPIDPSMFPTWPAKSEQQRV\KRGTSR PP\EGGLGYSQGLDDDLKETG\FHLTTT NPGGLLPRGPGFSLRVAEVSLEDPVIGR NSAGDHRRGYLPANWCDGTRNSSSYFVL PCFVVFVFLVCKLSRIKSFSLWRKELCF LRDLPRAEVRGIFRGAHVQGHKPHHPL PLSTRTGLGWAVIWKGTGGSRVDCLI FG AGDLFLCWDERCPLAPTHSSRPALSTTS PRPPTTQPQLLPAGLEQVFFYYKVGVLK CIKIFFEE
12978	26879	A	13116	469	202	MIITVGLCEYTKSAVLVQHSDDLPPAPG VFFLAVLDVVDIKIVVHPVFCFVCLYE MESCPVAQAGVQWRDLGSLQPPP\PGSS TSCF
12979	26880	A	13117	193	383	AARMASFFVFWFWFSTF\SLYSICVCV CVCVCVCVCRMHTVQLYFFQVGCQCSSL LNPLFPMN
12980	26881	A	13118	146	350	HYLVKFLLLAHPGSKAPPLNTLQPPPLA TREQPPLTVIFHYPTSYKMAP\PYLPS LTLFGLSPAPR
12981	26882	A	13119	124	254	HALLQTLRDLQAWHVALVIPATW\EA AGGSLEPRSSRPAAWAT
12982	26883	A	13120	150	45	SLPRLECSFTVLAH/C/NLHLLGSSDSP ASASQVVGGI
12983	26884	A	13121	336	446	IPLKISSWAQWLTPV/IMPAVWEAEAGG SLEVRSSGPA
12984	26885	A	13122	181	39	QNLTAQDGVQWCDLGSLOPP\LPSSWDY RRESLCPSSFFIFWKRWGFT
12985	26886	A	13123	463	2	GPAVPSGLYLKGPMMRLCASHSPESH HDKGGQTLPRIPQ/PLLEGGSR/PLAW GAVAGLPSNRPRIVPLPAPTRSGTRVRP HTGHQPGMSPGCGCESKWPMSAAWPEA YPHFLLPFPTQGCVELGPLYTADPWVI CVSLLPSCPNSSTAVDDV
12986	26887	A	13124	429	263	DHFSFLCVTGSQSVAGVQW\LIIAHC SLKLLASSDPPASVFQSTRITGPFLSFT
12987	26888	A	13125	310	486	NKKTTRGESSKQRPVSHHPGWTVP SGFTAASAS\RARVILLRPPPE
12988	26889	A	13126	124	461	GSPLQLLPSPLAALTRDCSEAPMGSCSV AQDGVQWRDLGSLQRLPPGFEPFSCLS TPAP\FPSGWDYR
12989	26890	A	13127	2	337	RGAAPAAAVTALAARTWLGVWGVRTMQ ARGFGSDQSENVDRGAGSIREAGGAFGK REQAEEERYFRAQSREQLAALKK\HHDE EIVHHKKELERLQKEIERHKKQIKMLKP
12990	26891	A	13128	681	422	CRSDRWAKEHRGKRGQDSSKDVMARLME APKQTAQYFFIFYFFETKSYSVTQAGVQ WLDLGSLOQRPFP\SSDSPASASCAPQ TAH
12991	26892	A	13129	299	579	LVMFCKVTKIERLNLWRPGTVAHVLSQ HFGRPRWAVHVGWGVDRP/RLTQHGTEP

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						SLLE\NRNISQAWWCMFVVPATREAEAR ESLEPGGQRLQ
12992	26893	A	13130	268	438	KVDKSMKMRKNRPKNAENSKNKKASSPP NDCNSSPARVQ/SWTENEFDKLTEVGFR KW
12993	26894	A	13132	1108	1529	KIHSSFVLLNAKLVAVAAKTPKFYKKKT DLPQTYHSAQTAVPEIPVSAHSTFIRSF IHSFIFETESYSVAQAGIQWHDLPSP GS\SDSP\ASVSRVAGTIGVCQQAFLFF V\FLVET\GSFPHLSPLTMIRNNKQLFK KGH
12994	26895	A	13133	497	370	RPSTVSPRLECSGLILAHCS\LDPPASA SQTAEITYGHHAS
12995	26896	A	13134	217	373	CNHTETIYVNNKKHRPGTVAH/SLYNPS TLGGQGGLITQAQEFDTSLGNMTLS
12996	26897	A	13135	257	507	PVSPGFPPPL\CPVPHTPHLCPPCRYPES PGQPAAQHCGAPRQPQPNPRACSSRGLF RCPPACHHAPSCLLCVCPPLPQCCRVQG
12997	26898	A	13136	137	309	PSFPTHQPFCFLFCFLVFETE/SSIVA QAEVQWCDLGS PDQSSASPPSASSLPL SIW
12998	26899	A	13137	297	419	GGSAVYYIWEIVQVLWLPVIPT\WEAY AGGLFEPRSSRPA
12999	26900	A	13138	213	492	QVGINYQPPTVVPVGD LAKVQRAVCMLS NTTAITEAWGLPGAISAKCALVHW\YV GEGMAVGGEFSEAREDLAALEDYETCGPW NPVETEAERR
13000	26901	A	13139	246	534	DRVLPPLPRLECSSAILGHCP/APASQV TGTGTHHHITQLIFLLYCWLCPPLASE ASAESPPLPRGFLCFSSTTSSITAIPA TTRDYVDVSRSGS
13001	26902	A	13140	1	206	SLEWPPFFFSFSETGSHSFTQAIQWCNH SSL\SPTSASQIAGTTGVHNHAQL/VFV FCFAFMSPQLNSNC
13002	26903	A	13141	164	582	GLVLVNLVLRSYLMVFIYINSRLQVTD ASRRERRENESSWFCRSVCRM/PPVGP SCVHPCSPRGSISPCTPHCPLKTTQAPA \PPRPLPRVGP GPHLDQSCCVAARPLYD PILVAHSSWPAPSPVPVPQEDTEHGA G
13003	26904	A	13142	235	367	LALNTFCWLGVVAHACNPSTLGGQGEV TRGQE\QANMAKTCLY
13004	26905	A	13143	91	403	GALQPATAPWEPLSGLAEGAISPCLQG G/SGGRGASENRGCTRPGRVPGRRILNR PRAWSSWPAPPAGSERPSAINCPRAEE CGRRVWDQAALPAAPAWVPV
13005	26906	A	13144	558	147	GHSFQNWLLGCPLQLQRHLLHPPDASEE CGSPFWTPLRPHIHPAGPHGSTHK\HA GGCLFPLRPSPTHPCGPPVPLPWSQ\QA PLCPHPPHSPHDWECDPGKSALIPPPA AQSPSRLIKHAANEPECSRNRRPGIP
13006	26907	A	13145	321	421	GCAQWLTPV/IPALWEAKAGESLLFRSL RPAWAI
13007	26908	A	13146	3	398	IELLQSHDKTLTDKLLLLDEQRKWFLE MESTPGEDVNNVELTTKDLEYHINLDD\ KAGFERIDSNFERVSAVG/KMLSNSIAC YREIFHERSVKVANFTVAILPQPHKLSV TINLIQQPSTLRQDLLAKR

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13008	26909	A	13147	228	261	SKTQRSSEYYSLSVCVVCVRVCIYIYI FFFFETEFLS\APQAGVQRCDSLRLRP PP\GSSDSPFSTSQSAWDYRREPQRPTS LHYFVQLKHNLRVVKRRDLRNTTR
13009	26910	A	13148	3	275	KHLSDLQILRLGLSSKTRKTRYSHFAQG RSIFFLLRPSVDWIKPACMDGNLLFSKF TNLNVNI\TKKHPHRNVQNNVWPNVWAP WPKEVDT
13010	26911	A	13149	218	382	AWDHIKLESFYTAKETT/RMKRQPTWEW KIFANYPSEGLVTRMYKELKQLYRKKI
13011	26912	A	13150	391	29	FCFLFLFMFLFFFEMQDGVQWCNLSPPQ PPPPG\SSHSPASASQVVEAENCLNPGG GGCSLGDRLRLPQRKRERERETERKRKR ERASCAFCGAITFVNMWCQKHHTCNHLP WLTVFETNKL
13012	26913	A	13151	351	157	FGYSRFLCVYINFRTNLSTINYICTIYIN LYL\NIHTYTLIYTVVHTYTHIHPYIY IGILTGIT
13013	26914	A	13152	402	111	TFFGGEKPPFTLRPGPPRREGGGGPPGP REGGFFRVPLGAFGPSRPK/RPEKSGPV WAPQIFLWGGKSRRAIKESGKGFFSRIT LLVFATEKKKKTTLF
13014	26915	A	13153	310	141	REHEKQKPLSQVRWCTPLVQAAQAEAG GELEPRSSRLQCSMT\TPVNSHRPPARV T
13015	26916	A	13154	153	21	LNKCVISWLGAHAHACN/PSTLEGRWIT QGQEFKTSLGSLAKPHLY
13016	26917	A	13155	429	275	SVDIPLEKTLINKDVFEAAFKCKVS/R QARVKFKKRYKPVKTWFFQKLWF
13017	26918	A	13156	303	42	YRERAPVYPIIINIAFGPHKQ\TRAH THHTRMHAHTHTHPAIIPAFANGLGT FHHKGRTYNDKVKPRLSCEAAIPSNLKS REFR
13018	26919	A	13157	198	13	SHGVAILLFFHFLNKRAFT\YSPAMNSS LCEIQEPSLG\SGSGPLSGNRMSGKGR KYFAKI
13019	26920	A	13158	192	2	ISNSHRKDIKDPEVLLIEQKYILSGQMQ WLTPVIPAL/V/EAEAGRSLEFRSLRPA WATDRDSVSK
13020	26921	A	13159	40	190	RVDPRVRESRSVAQAGMQWRDLGSLQAP P\PGSRHSPASASQVALFLNRK
13021	26922	A	13160	1	178	PTMVLSPADKTNVKA/AWGKVGAHAGEY GAEALERMFLSFPTTKTYFPFDLSHGV SSYL
13022	26923	A	13161	411	41	ESLQICVGLHAKPSWDACRPWLQAWFR YFLLTFLGPLVFLLVWFWSKIYFLYHLK NPSLSSCYNLD\FNTQYLKYCKKKRLG AVAYACNPSILGSQGRITRQGFETRL GNMAKPDWVDP
13023	26924	A	13162	372	218	FWKRSWISKKGLFKRGVSLSLSL/CDT HTHTHTHTHTHAHSGYLCVLRKVK
13024	26925	A	13163	247	89	QGLVLSPWLKCRGGITAHCGLLGSSHPT TSA\QVAGTTGTQHHAQLKFFILIIL
13025	26926	A	13164	122	409	FPSTAIANSH/CSSPQGC SAYGVAIRLF LRSSNKLAL\LYGLAL/NSFFCNFQEPS \LGSLSGPLSDNKSNNLCCFKSPSSWLF AIAVLGNYYSLNTRVSGRRDPGTPNACS
13026	26927	A	13165	69	313	PSVSLFFPPNHNIVIHMLLKINSIFGE

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						GLALSSRMESVTTITVHCGLDLLGSGGP PSAAS/RVAVTAGTCHHSWLMFLSFV
13027	26928	A	13166	310	26	IKSMTPLPALNVSLSYLLPPLRPCRERG MVQDRFFCFLFCCCCFIFSETGSHSAAQ AVSQNKKTGWAWWLTPTVIPATHEAEAG \\ESLERGRQRLQ
13028	26929	A	13167	296	68	KNGPLNLATKSLILTMKCLGVVLGGKP NCSKLKKNKIKTKKWGWAPWLTPIPLPA/ LLEAEAGRSLEARNLRPVWT
13029	26930	A	13168	2	235	GATPCPREPSLFLPLAGWAPLSCWAPPPH CTQGTTPPGLMGTG\\APIAIIGGNARSP PMFPLPLSGTRRALSQAECPTF
13030	26931	A	13169	248	406	TERCGFDLLSLGQVQWLTSTVIPALE/EA EAGELLESRSWRPAWATWQNILSLKK
13031	26932	A	13170	33	308	NSLQGAEMAAQSSLSFSASEG YRGERGR GRGRGRPGRG/RSEGRGGRGRPGRGGRG RKVLLLRICVWRRVRLWNRGRIGVGGR VTYLMSEI
13032	26933	A	13171	294	56	ICKRNYLFFIYFLREGLTLLPRLECSGA ITAQCSL\\GSSDPPTSASTVSGTTGACQ CALSSRDALISLCYPGWQAAPGLK
13033	26934	A	13172	71	476	DSLNYDNHLYQMPLIYINMGLAVTISLL G\\ILVYRSHLISLLCLEGIILSLFIIA TLITLNTSHLLSNIVPIAILVFACAA VGWEECGFRSRPTALILEGPLRSCQPR CVRPACTRRGPAFVGKNRHSIGG
13034	26935	A	13173	86	318	NNCNVVCVCVCVCVCVCVCIHICIYV/YV YICIYTYKYICITYKYICICVYIHYVM YMCVYVYICICMCVYICIDSKGR
13035	26936	A	13174	466	726	NCMKFGAVTRIG\\DLFWINPLSSCSLL REKDPPTTSGPQTDQPKHLTNFKSGKR PLFTLFSNLPHYPSTSFBSQSWRHTSIS PFS
13036	26937	A	13175	128	325	FLRVILICHKMYGCVCVCM/YACICNGM CIYMCVCVKSWKLKPELKCLCISDEVGW VLTQWAGREEN
13037	26938	A	13176	134	311	INSNSEKMGSHYVAQDGV/WQGLFTGH GIAHCNLLKLGSSNFSASISQAGTTGI VANG
13038	26939	A	13177	577	1052	SPTSTRTGSGVAMWLSQPMGRT\\CRSKV ASKSRLHGPLIAHPPIVRCPLRHHY\\ KAQAGRGLSLEE\\LRVAGIYKKVAQTIG IS\\EDARRRNQST\\QALQAKVQRLK\\ED RSSLILFPRK\\PLAPKKGDSSAEELELD TQLTGPEMPIGNVYKEKARVIAD
13039	26940	A	13178	496	678	TLNFVWAQGLKITRPWKNAPVFPVW\\R LRRKNLLTLKGEICSDPKWPYCLPPWKT KKNLV
13040	26941	A	13179	192	421	GIYTFFLSFFLFLRQSLTSPRAGVQWC NLCLPGSSDSPASASRVPG\\ATGT\\CHH GSANFLYFLVGDRVFGVVGPR
13041	26942	A	13180	144	5	LQLATKLLKMRLGVVAHTCNPS/TLGGW G\\GRSQGQEFETSLANIVKP
13042	26943	A	13181	351	51	KKKKKIFFGTKRRRFFFLKGVWGPPPPK VSPPPPKISPNPPKNNPLLKA/IKSPQ NWLFFFGPPSCKFFPPFLNPKNSPWEN PPSGGEFSPKKKKKSAI
13043	26944	A	13182	2	218	THFGCFVFLFFETEFCSCHPGCAGVQW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RD\LAHNSLLPPLG\SSDPPTSASQSA EITGMSHHACPIFKKHS
13044	26945	A	13183	33	304	EKHGIFRAVKILCMILQRWTYATHLSRP TGYTAPRVNPKLWTLGDNVSM/SGSLI VTNTALGWGLLIRRSSACMGQGDGMNLC TFLSILL
13045	26946	A	13184	277	13	FSFFLIVEMGSCYIAQAGLELLGSSNPP SSASQSAGITGMSHHPAWLATLKRAFVS D\NSLSFPSSSENAHLSILAGHFCLMGFF FFQ
13046	26947	A	13185	140	361	ITCCCVCIYTHIHTYVYVCYIYTHTYI RVCV/YIHTHTYIHIYIHVFIYIYIYT FMHTYIYPYVCMVLLQLTL
13047	26948	A	13186	64	759	CLSASAPTSTMPMTLGWDIRGLAHAI RLLELYTDSYVEKKYTLGDAPDYDRSQ WLNEKFKLGLDFPNLPYLIDGAHKITQS NAILRYIARKHNLCGETEEBKIRVDILE NQVMDNHMELVRLCYDPDFEKLKPKYLE ELPEKLKALTS\EFSGGKRPWF/SQGD KITFVDFLAYDVLDMKRIFEPKCLDAFLN LKDFISRFEGLKKISAYMKSSQFLRGLL FGKSATWNSK
13048	26949	A	13187	41	426	LFFFFFFESGPCWVTQAGRR/WNDHGS LQPGFPGKLGSPCLTLRSDWNYRPGMCRH TQLVFAFFFFFFPREKKFLLGAPTGFKTRG LRGPSRFGFGKGNKGQEPFPPRAKGLIF LEPERGQAFGTVFFGPTQ
13049	26950	A	13188	39	197	FFFLFKTRSCSFIQAGVQWCEHSSLQPO TPG\SSAAPASASCKAGTTEAALKL
13050	26951	A	13189	221	396	GIQLQGAELWDVTNSPFCWRLYDQKTV YHECRMWANSHP\PPKGLLRDITPRCW AP
13051	26952	A	13190	2	826	PGSTISSRRRGACGSRGGHFPSPRGGSG VASLERAESWSTEPAKAIKPIDRKSVHQ ICSGQVVLSTAVKKIVENSLDAGATN IDLKLDYGMDLIEVSGNGCGVEBENFK GL\TLSALKHHTSKIQEFADLTRVETFG FRGEALSSLCALSDVTISTCHVSAKVG TLVFDHDKIIQKTPYHPRGTTVSVKQ LFSTLPVRHKEFORNIKKKRACFPFAFC RDCQFLEGGSPAMLPVQP\AKLTPRSTPP HPCSLEDNVITVFSSVKNKGPGSSR
13052	26953	A	13191	235	1	SPCARQCCPENPAGQEPRRRLRGPCKW WPRSIKFPLPAV/RARFLLPSAPLRQL VSGRVGGRVGRPGKAVQVSGGLN
13053	26954	A	13192	2	386	VIYLLFFETESCCVAQARDGVSPCWPG WFQTPG\SSDLPASAPK/VAGITSVSHR TRPDVRGFKK/GLQLEMHLALL/TT SHRFWYFVLLFSFVSKGFFIFFFFLFFF FFLGKGGFFFFPRGGGGQI
13054	26955	A	13193	749	506	GQTKAFVLSYCGASPSIKQ/PCPQAKDH PLEPSMHPEGTQLQSCSTMLGPRQLSSE KQPLLPPRSHLKSSPMLRACKGLTS
13055	26956	A	13194	73	297	RMPGFGALGSPFSCQRIECPC\AGAGSC TYASFCKCKEYKCTSCCKSECGAFPGNQ GAGQSQRREPRAQAGAGQ
13056	26957	A	13195	670	390	PRETYIKPFARSIGCQPPKTIHPTSRRP STRPPARPHARPPVHTP/APSVHMSDRP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STCPPSIH\RPPSTDVSRPQYSLSPSTS LALPGQSC LGR
13057	26958	A	13196	2	438	LSFTSIEFCHLLFLNQLICNYVIFTKSS TISCEALGRLLVVYPWQRFESFGDLS TPDAVMGNPKVKAHGKKVLGAFSDGLAH L\PPLKPTFATVSELHCAKLHVDPENFT LLGNVLVCV/MKHNFGK
13058	26959	A	13197	57	499	SPSWPRSSARPCSGHCLLPGLWDHGKAP CLRAARHSQGHGFRKGRKGCGLWAAGW TKNPVPTWRAG/SRRGPGVTSPPPVPSV QNPP\PQRRHGGSQATRPVLFPTPPKH MEGPNAPILGDQRITAPPEILYRPPRA ATCDALRRG
13059	26960	A	13198	34	465	GILPYSPCVLRAPNSKRVRKCGCTTPRH L/CKATRKCGCTTPRAPLNETRKCGCTT PRHLSRQLGNAGALPRGHLNETRKCGCT TPRAPLNATRKCGCTPRHLSRQLGNAG ALPRGHLPLKETRKCGGATPADAFYETKK IGGGL
13060	26961	A	13200	177	1075	PTSSSMFAFKKKLQGLVAATITPMTENG EINFSVIGQYVDYLVEQGVKNI FVNGT TGEGLSLSVSERRQVAEEVWTKGDKLD QVIHVGALSLKESQELAQAHAETGADG IAVIAPFFLKPWTKDILINFLKEVAAAA PALPFYYHIPALTGVKIRAEELLDGIL DKIPTTFQGLKFSDTDLDFGQCVDQNRQ QQFAFLFGVDEQLLSALVMGATGAVGST YNYLGKKTNQIV\EAFAQKDFSLALNYO FCIQRFINFVVKLGFGVSQTKAIMTLVS GDSNGPTPASTCRKPPGEFT
13061	26962	A	13201	35	464	VQEFKTS LGNVAKPCLYKKKKKKSPLGG GVPPPPPKKTWVGTTLSQKIRPAGPLIF PPPLPRGQQGEPLSPIKGGGGGSS\YP PPPPCPLTGRA/PPSPISAKSSPSPPP CQYVYHPPLPLFFFLHALRRATAPLFL FLVRA
13062	26963	A	13202	1153	259	AGGVLRLGVVTGSRMASDSGNQGTLC TL EFAVQMTQSCVDVAVRKS LGVAGVQDV EVHLEDQMVLVHTTLP SQEVQALL\EGT GRQPV LKGMG\TGQFSESGGQPV AIPGG GLGTVQGVVRF LQ LTPERCLIEGTI\PG LEPGLHGLHVHQYGDLTNNCNSCGNHFN PDGAS\HG GPQDSDRH\RGDLG\NVGAN AAGGAFFRMEDEQLKVWDVIGRSL\IID EG\EDDPGAREGQSLYPKITRELPGSRL SCGI\IAKSAGLFPEPQSKICSCDGLT\ IWEERGRPIAGKG\RKESAQPPAHL
13063	26964	A	13203	281	420	VDGSKKYNE MPVIPALWEAKAGGLL\EP RKSR TAWATREDSVSTKN
13064	26965	A	13204	3	1125	SDSPQTPRMV MAPRTLILLLSGALALT ETWACSHSMRYFYTA VSRPGRGEPRFIA VG YVDDTQFVRFSDAASPRGEPRAP\W VEQEGPEYWDRETQYKRQAQTD RVSLR NLRGYNQSEAGSH TLQWMYGCDLGP DG RLLRGYDQSA YDGKDYIALNEHLRSCTA ADTAAQITQRKWEAARAAEQWRAYLEGT CWEWLRRYLENGKETLQRAEHPKTHVTH HPVSDHEATLRCAWLGFPYPAETITLWQR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DGEDQTQDTELVTETRPAGDGTTFQKWA VVPSSGEEQRYTCHVQHEGLPEPLTLRWE PSSQPTPIVIGIVAGLAVLAVLAVLAVLAV MAVVMCRRKSSGGKGGSCSQAASSNSAQ GSDESLIACKA
13065	26966	A	13205	417	13	GHPRVMLQCHMGASLSIMTPPPPIRSYQ PALTRSSATKPA\TSAPSITMTPVTAN IS/VWPTANTTTTKLSNPTSS/STLSTP IWHPSILPAPPSTPAPLTTVTNSATTST ICFHVQLFQAHHCHHCIAAALEYTS
13066	26967	A	13206	1139	559	GLSELSIHPSVARVQEGHATPERSIPW PGGKPRRGGRGTGLREWGGGSHRSLGQT KKKGAKAKRDHCAHGPAAAFQGGFFPRAT QLLSPCHGCSWKENQPP*GPPGHACTAW EKTVTGSCRVPVTKPSDPGFVQAPGT KGNPAPGMDGCAGFRISCHFPVPTKPLS NTGICVLLCYEFGFLIAIVGCWGFK
13067	26968	A	13207	306	332	ENGEIRIYIYICLYLIKHWEEAGCGSV HL*SQHLKRLKWEDYLRPGVPDQPGQHR ETPSQKLNK*INND
13068	26969	A	13208	48	233	GKQNHLCCLWCRLFLLSAVISRNVTIL T*LSLSLSCVCVCVCVCVCVCVCVAIL ENYPR
13069	26970	A	13209	250	2	YCEGDLGSSRPGVSKREFSPRRDKRIM PWPGAVTYAYNPSTLGGRDWIA*A*EF ETSLGNIVKPHLYTHTHTHTHTHTH
13070	26971	A	13210	615	120	SVFWPLLGGVSWSGYTEVRGPLEKAVCP LSELEYCAGRSAALFRAIRLFKDALSLL KLCPPPPFPLGAPLSP*EALVCVPLHV STCLS*WCPTPCPPERSWCVLFPSPMYPR VCPDGLLPVPLRGPVGVVPLHVSMLCL LSLFNSLLRLRTCGVWFSVPVLVC
13071	26972	A	13211	239	429	FILLRNKLQPGTVACGCPNSTLGSQGW IA*AQGFETSLDNMVKPCFYLPQLKKKK KIKNLGV
13072	26973	A	13212	954	503	VQLLPLCGRDLYLFAFNLPYRCWQHFL SKPRAPILAGGSDRWPCPCFWLP*WC HVSAHAPQFPCKAPEAPLPVGCPCSPA PSLEAALLILRAGLVVLRAPFCFSAHLL SCHSQCCQFPCSEKRSCLGGRDRHAASN PLSAVWPPGE
13073	26974	A	13213	1844	1147	LHSQIYSTAKKASLSMKGSRDKTRAASS RPVPSVLGVPPWSTLLQHPQNMWPGPAQ QQGQPSGRQAWCTPGEAPGAEEAPQ*QP HPEEDHSGGPQASALALPPSPSQRDV QGETGMQGRSAPRSASSSACCACRWSRL PCPQLLQRHPGLRLVSPAHSRPPGPAPS SSSGSLVPGYLPQKGLAGLSAGAVLCP PGLLRVAHGAGYGPSAQMLHARLSSSSL RGKRFLRF
13074	26975	A	13214	413	60	LCSKSCCHGSFAMDCETLLTFPRLFYPIL HMPTVPGQALPVHTPFL*LKLPLLP SCHSPLFLD*AQESPPPGGLFGHPGSG VLCLWFHSLKHPVLSGSSVSTPGSASPS RSRAL
13075	26976	A	13215	67	196	GLSLSSPKVTHNATLMGCIFQNKAFVY HSMKQKKIILLFNMA*P*YPLDFGEQWP LHGSAYSTIL*LDLFCKKEE*DEIPY

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						V*CFMLLWKSTTM*KKIIILFNMA
13076	26977	A	13216	161	2	SVFFLFIDRRLYLKSVWAAVNSSTLGG RGRRT*AEFKTSLGNKARPRVYQ
13077	26978	A	13217	57	184	CLTVCKDKVSLCYPGWSPVV*SYLTAAS NSWSKAILPPQPPE
13078	26979	A	13218	292	400	LKVKQGRGHLDLNQGPLDL*SNLPLSH TPSHRTV
13079	26980	A	13219	186	394	YLVLSFLFYFLFIFLSRVSLPIFFILEI *LGIVAYTCNPSTLGSQGRIA*AEFD TSLGNIVRPPSLI
13080	26981	A	13220	315	448	KTCDLGVVDHVYNPSTFGG*GGRIT*GQ KFETSLDNRRASCYK
13081	26982	A	13221	3	13	LRPLRSFVSVRLWASCCLGSELVVDKT KRKKRRELSEEHKQEI KDAFELFDTKD EVIDYHELVKAMIALGFDVKKADVLNLI KDYDR*VIGKISFGHSIEIVTDFQL*R
13082	26983	A	13222	1	715	VDMHSRGSPELTHASTHASGKMAAPWAS LRLVAPMWNIRIRGIHRLGAAPVPEGNQ KKKRTILQFLTNFYFDVEALRDYLLQRE MYKVHEKNRSYTWLEKQHGPGYAGAFFI LKQGGAVKFRDKEWIRPDKYGHFSQEFW NFCEVPVEAVDAGDCDINYEGLDNLRL KELQSLSLQRCCHVDWCLSRLYPLADF VAGAFRWAGCPRI FRTGAKHGFFHLQ*D LSSGWATCPGTSPT
13083	26984	A	13223	1019	1238	LTGAEYKKSDDLTESVTANLEPEAPKVF SRLDDEAPVTVLPARLPLPAP*HTARPD PPQRRRSMQLAPARPL
13084	26985	A	13224	1534	1181	RWNSEPDYSAGGPRAGRCARLLPVPKSP GGGGAVAPGPTPLRAERTAVRLSIS* NSSTAPADPGAAPLHPQPAEAGTWVSA FLRVIFCFPSLGFGCWEKKIAFVFPFPT DEKCL
13085	26986	A	13225	328	22	CLSPRDRPFQGPAPFKHPPLAFLSQ PGKVQYFFESNCKSLSSQEIKNRSRVPT SPPAPSPPPFFLYFSLTAEGGEV*KET LSDRAPPSREAPICQV
13086	26987	A	13226	180	5	NSIDYKINVKNSNRPGAVAHTCNPSTLG SQGRRIT*AKEFETSLGNIVLLIYIIY YI
13087	26988	A	13227	237	528	VGLCQDPLLLTLTDSFCSVLWGGSHLAF HKNLYVVHIDLVMYFSRISFYFTLSAAI CLSLYLGSILSPFL*LFYCAVTTLYLC LITTLFFLIPKV
13088	26989	A	13228	140	366	NATCLWHPMSFYAPTY*CLSPGLLRVW LAITPIVLMILISSYNHVISYGGTFRS NFFLDQIILTFLIYELHIV
13089	26990	A	13229	257	25	LPAHSLGRDLAQPYSMRPPGGELRAEG QSSLCSVARSSL*LHVCVCVCVCVCART CVNVFACVLLSTKVCCLHPLPE
13090	26991	A	13230	561	52	WPSCSSSGSPMLLPPVPPGSLG**SFSP LPAAALPAPCAAPRAPLRPCGPAPT AAPAPAPAAASLSAARAAAGSPGSR PSARGARRRSGPCAPPEPRLGPRAPSS APRTRTPS*GRARSGGSAGNAPSARRT QGPRAACSLARSWIWPAGRGSGCRAL GA
13091	26992	A	13231	335	103	CQKYSTSYCNKWLATLVITCSRKI*DGL



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						KGQAWLVPVTPMLWKAEAVGLPEARSLSSPCNMARAPALKKIFLIGQV
13092	26993	A	13232	452	712	VGLEGED*PPFSPAQSQSLSCWPDSCPSWPPDQRPGERPQPPDPESHGAEEGLPERPSDA*ARPQPFSLHPGVFPQNASTQ
13093	26994	A	13233	480	2	SCFSEDWNPLKFKLQLSTSLSYRKSHTLHCAHHFRGQCHSD*AFLVFSLTCLQVGLSLRFTAGDVSPSYPEKLRVL*EGRVADFHV MARKGQQAALAILLQNARTGYVWWLTPVIPALWKAKASGSVKPRSLRQTWQNGETRLDRGESASQSAGMTGM
13094	26995	A	13234	692	824	QIMALPFPSPVPPLVM*CKGGKIPPPP SKNPRTCVGNVTIIKA
13095	26996	A	13235	657	872	PRGPRLDVLYACEPQLITCLELGTPLKVRFWLEVVDHTYNPSTLGDQGGRTA*GQEFKTSVGNSKTLSLKKK
13096	26997	A	13236	168	365	QESLCILQTCTCAHQNLK*KFGGKSRLG AVAHACNPSTLGGQGRII*GQEFETSMVNMVKPYLY
13097	26998	A	13237	31	338	WYIVYICVVCVCYIYIYIYIYI*YI*YIYIKHTVQ*H*HLAFTFTLLCNCHHCPSLELFHYPTLTYHTH*IITPHCSSC*YQLFYFHLVYFVDYSRYLV
13098	26999	A	13238	714	1001	SSGVSCLNLRAGWITGVNHHIHSVLVLLKREK*TONIITEVCLMFLLLPHLAIEATVTWPGMVAHACNPSTLGSQGRRSV*AREFEFLDNIARPCL
13099	27000	A	13239	250	406	NLA*HGGVHMWSSASQVAGITGTRCHAQLIFIFLVKMGFHHVGDGLNLLTL
13100	27001	A	13240	256	193	WINFISLPLSSLT*TLSCVCACVYVCV CVCLRPCVHIVGGNLKRYIVFARSVTLGCKFTHLHISLIINNDT
13101	27002	A	13241	1	257	GMDLWQMCHSLSLPLIFFFFFFSEKTRS NFVPQAGFQLRALRDP*ASREAGITGLTHHVRPGQIFKKIGTLKPTILLPLLP RK
13102	27003	A	13242	319	406	KRGWT*WLMPVIPTLWEAEBAGGSPDVRS L
13103	27004	A	13243	228	56	KGAPPVLKPGYPKAAKNPTPFKPPGSKV GENPPLF*NPCPGGNPPTFFFFFFFFFFF
13104	27005	A	13244	1687	612	ILGNQCCKFDAYNALANESTMISIKLNE*VREREREKEKEKERVREKEEREKKLTSSKGTGSTATFHV
13105	27006	A	13245	220	1	TKDPSSTMPPQPNPLLSFKSQIFLIFLFIKKYVGWMQWLLPVIPAL*EAEAGGSLQPRSSRPATWRNPFI
13106	27007	A	13246	204	375	ASWPPGLQYELRIIKCLLHCWTRAMIFRERERERERERERERERE*VHLKRKGA
13107	27008	A	13247	158	2	IWVPKETFFQNFFFFGKENNFNGFFF FFFFFFFF*DRVSLTLHPSLGYR
13108	27009	A	13248	221	3	NPSQGFPLLKIFFFFLRWSLALSPRLE*NSI*KN*KI*KISWAWRTPVVPGAWEAEPGESLEPGRQLQNE
13109	27010	A	13249	81	341	GELNDTIHVKYL*YIKVL*RNRTNRVCVCVCVCVCVYACTQKDLF*GTGSCNC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GALVRPKSARQASRLKTQKTVVIRSLKAVC
13110	27011	A	13250	299	1	ATARLRFLHGAWWYASVVPPTQEAARGFLDPRSSRME*AMILPRTCPTASVTDKIPSLASQIHRPSRVACVILLSSHAPTEAPSRWPPPSPLCPAGSRA
13111	27012	A	13251	106	146	LCVLKQVKQATWTKYSSSQIFAILDCMTLSSHPALKYCNYVLISNQSPNHLRL*CSGMISAHCNLCLPG*SNPASASRVAVCFKASQASVLD
13112	27013	A	13252	217	158	LFEIFCIPFFFFFFFNFFFETRSHSVSQAQVQWCKQGSQIPINFFWGKEGVIDKLILISYGNAGGFKVAVTPVCTTALQPGRQSETLSQKRN
13113	27014	A	13253	150	56	TILILLLLYETESQSAQDGVQWCDLGSIQSPPRSSCHSPA*AGVNRLRQENGMSFEAEIVLSPDRTTALHPGLQIETLSHIIITILILSTISFHQLLH
13114	27015	A	13254	174	145	PCLKMTTYDFKSALEIAFFCFTAILRYKLLIKVTHFKWLRVAHDCNPNTLGSGGGRITWGHEFKTSLANMA*PTTRSYSQRVGIMGITIPDEVWSRTQPSHIRSGPSKVYP
13115	27016	A	13255	179	273	GQWLTPVISAL*EVEVGGLLETRSLKQAWAT
13116	27017	A	13256	264	382	GLKIGKGCSSWFTPVIPITL*EVKARGLL EPRSLKSAWAK
13117	27018	A	13257	1199	1563	YLVVGPAPVPLDLEPGQAGATCGPVSHYKIFAKLWAVGSILDLMGPPE*GSFLSVFTSLCFIYGVTPPHFSEQPHPASPSASGLLLLKGRAAWLVSTLCIGSPAPMLTGIFPHKVYNQLFI
13118	27019	A	13258	194	242	ILYVETGSHYVAQAGLELLGSGNPPASTSEIAGIEA*ADEFIYGVSWQDECICKSMKQVAHASIPASEVEAGGLEPEPRSSRPA
13119	27020	A	13259	322	120	GPTFVLDAFQKLCLSFTSQQADGIIPA FPIRKQGGTQWPKPVIPTLWEAKAGRFL*PRSRPAWAT
13120	27021	A	13260	237	1	TSKKISLGWGWKGQIPGTWEG*AKRPFEPGKPRVQWTVQVPALDFSLGGKARLCLKK KKKKQKQKTLKLC THSRITYSRA
13121	27022	A	13261	52	318	SAVGIIHRCDGSH*P*TPHEKQLSFLSLPSSWDYRGITRELFQRFPPWIFLQLITAVISSESTVLKNLELAARGSHVRVIMMAVPINPF
13122	27023	A	13262	274	1	KKKKNSPVWWTPVIPGSPG*AGELLEWRQKVQLAQVVPPLAKVVPQTKVVQGCPLALQPGEHQGI FVSQKKKNPKTKRKYWALFCSLPSC
13123	27024	A	13263	717	877	NSTKEMAHWPGVVAHTCNPSTFGG*GGWIT*AHEFETSLPNMVKPHLYKKYKK
13124	27025	A	13264	288	131	SLYIWHSKRLITITNNKISGVWVCLPVV SSTWEVEAGGSLEPRR*RPAAWTK
13125	27026	A	13265	80	287	FMNGEAS*KTSILSQAWWCAPVPAAQ*NEAGELLEPRSEWLVAWATRALRISSRGLRFRFLRRFTSTR
13126	27027	A	13266	3	241	VGLFLFFFETESCSVTQAGVQWCGLS*L*PPPPGIRDS PASASQVAGTTGTHHTWLIFLYF**SSGFHYVGLGRSSNS

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13127	27028	A	13267	103	359	ICVYVYVCIYVYEMRATSKDFLNQVWFS FLRTVAVLFEYLIIVL*MWLSFHIHIYI HTHIHIFIYVYTHVLIYVYIHTYSYMC HIYI
13128	27029	A	13268	172	12	SARSSQAIQIQKSVTSGQVKPQW*QS*P TPFLPTLIALTTLLLPISPFILIL
13129	27030	A	13269	2	203	RIENIRSYKNLAALFMTAKKMGTIQMPH NFEWINKMWYIHTLEH*SDKKKKKKKVN RAEIPKLIQK
13130	27031	A	13270	236	365	KIYRQGAVAHTCNPNLTGGQDGWIT*GQ KFETRLANMVKPHLY
13131	27032	A	13271	371	15	QNQINFALILIIINTLLALLLIITF*LP QLNGYIEKSTPYECGFDPISPARVPFSI KFFLVAITFLLFDLEIALLLPLP*ALQT TNLPLIVMSSLLLIILALSLEY*LOK GLD*AE
13132	27033	A	13272	2	16	PRVRTSSRSRAALELIFFFFLGPPNLPV YNGPLGRTPKGTGELDTGGSPILCVGQG RHPYWKGAAPLAPFGKGGP*GTRPLA GPIVPPKAGLQSEMPGMAPFCGSFG*PT RPD
13133	27034	A	13273	329	290	SSALVPRLECKGIFSAHCNLCMLGSSNS PTSASRVAGITGVAGQATDKTPQTL*RS SQPSHMDPVRVVS
13134	27035	A	13274	175	13	APCDHRPCPPENNPL*L*FSITFPNPIK RPHPYLLTLFSDSAHLHPGEIEQR
13135	27036	A	13275	355	861	PLTTTPAAPRAPCPPSRLSGQPLTGPT GSRRLSPNISEQGEPLALTVGHPLST QPGPTVPSELEPIQGPRG*GDCPTPSQS A*GGVLSCTPESHTFKPPPTGGRRWA RLGLNGAT*GREEPLQTRLPAEYPGPGP IDPLQPPP ISTASMATAFSDFLLLGRDP A
13136	27037	A	13276	865	667	KFLCILLDFLFFIF*EMRSQHRLECSA IIAHCSLKLASTDPPTSAS*IAGFTGM CHCAQLFLTF
13137	27038	A	13277	103	375	WSRRLPWRRLGYIELFQGLEIRHHFLF GPHYLRRTOCQGPVIPS ELDGQWDYMS PGV*DQPGQHDETPSLQKI*KTSSAWWH APVVPAT
13138	27039	A	13278	177	3	QQTGSRHSNSHRRPGAVVHASNPNTL GGRGG*NI*SQKFKTSLVNMVKCLYGR V
13139	27040	A	13279	379	372	SR*WVCMAHACDPSILGGQGGRT*AO EFETSLRNMVRPCLCLGNTNIYIYIHTH TYIFIQN
13140	27041	A	13280	83	1184	PPAHAARASPPSYTWLCYEVKIKRGRSN LLWDTGVFRGPVLPKRQSNHRQEVSSWE CRKHISKMSGGGLSTVYFFHRRFQITWF VSWNPCLPCVVKVTKFLAEHPNVTLTIS AARLYYRDRDRWVLLRLHKAGARVKI MDYEGERCGRGQSGMTGRNSLRDGI CNA INYASLHRTLKEILR*GSPSGLIVSLLS PPAHPPEDSPGNESWLCTMEVTKHSA VFRKRGVFRNQVAPKSYLHPK*ELSSWE RRKHNT*HTNYEVTWYTSWSPCECAGE VAEFLARHSNVNLTIFTARLCYFWDTDY QEGCLSLSQEGASVKIMGYKDFVSCWKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FVYSDDPEFKPWKGLQTNFRLLKRRRLREILQ
13141	27042	A	13282	1558	1824	SFPYLASFPFCLGLPLETLFHPGL*KD *SDTHTHTHTHTHSHTHAHFSPFPDP LFQSSPFSGGFIDEYKYPHLWPVMSVTC CRFCV
13142	27043	A	13283	1	519	PHFFLPQGFWGFSPFPL*KSSSPLKAL IFLGGFSPFPFPPKRRFSKIPRGVFFP PPKGGKFFFPFG*IWPPQGFLLKGGPS SSSSSSSSSSSSSSSSSSSSSS
13143	27044	A	13284	349	159	CPLEPKKNYFPCFF*ETGSCYVA*AGL VLVASSNPPASASQIAGIQGTSRHAQPC RIFLSKT
13144	27045	A	13285	748	869	WLGVAHACNPSSSLGGRGGQIV*PQEFETSRGNMARPQSL
13145	27046	A	13286	315	410	VQWFTPVNSALWESEAGGLEIRS*RTTWAT
13146	27047	A	13287	355	499	ARCGMHLYSQIFGRRLWEHCLR*KVLS QVWWHAPVFADIWEVEVGALLERSRL *CAMLLPVNSHGPPPTWAMQ
13147	27048	A	13288	880	701	KSYFSSHLHFEGKKCVSSILD*SILVLM CSWLMNYTHHTYIYIYTRTHICVHVYV HNF
13148	27049	A	13289	379	434	KRGPPPPKKRGCFSEKFF*GPPKTPFF FFFPKKKKKKKKKKKKKKKKGGRSRS RLADAWADAW
13149	27050	A	13290	253	344	GLFYNLQKIKIFYVKNLFFFFSNSITEA GVQWPNLGSLQPPPSGNSDPASE*RIV V
13150	27051	A	13291	561	745	AWEPSLVGETNVNSFNQYINWPGAVAH TYNAGTLGGQGGWIT*GQEFETLANMV KPSPY
13151	27052	A	13292	289	2	TLPQGEDFNKFVFGSIKQLQINL*NTD FIGNVFQSWAQYTPVPPSWVAEVEGS LAARSSRLCTIITPLNSHCSLAWATQQ DPAGRVGRPRV
13152	27053	A	13293	281	229	LKNKNVNKEKLRQGVVAHACNPSTLGGR GGWIT*GEM
13153	27054	A	13294	276	441	GLEPKFLIQKINQNWPDVAVHAYNPSTL GVQGRWIT*GQ*FKTSLANRGRKSENK
13154	27055	A	13295	258	389	NMVEKRLGQAHAYNLSTLRGQGERIT*A WEFETSLGNVVRPCI
13155	27056	A	13296	358	353	SFLAFFNGAFLPLRGFFWKTFFFGGVCW RRPPL*RKKKKKKKKKKKKKKKKKKKE MFKRNIGGEERGGG
13156	27057	A	13297	196	1	LMGKAPFLGGFIPPAPFFFLKKKKGGPG AVAYTCNLSTLGGRGRWIT*GQEFETSL ANIAKPCSC
13157	27058	A	13298	182	436	GVTILNVRHRHRKKVTLYRDLKKVRKCP KLHGNLRKVFQAEGIASCKTLKGHVWWL MPVIPAL*EAKMEGLLEARSLSAWATQ
13158	27059	A	13299	334	440	RHYWLN*AFYHSSLAAPQGGGHWPFP GITPLNSLHVPLLNTSA*LASGV*LT*A HHRVLPNNRALIIQALRITRILGLYSTL LPA*KNFAPFTISDGVYGSFAFF*ATGC HGLNVIIGSTFLTICFIRQLIFHCTSKQ *LWLEPPAWDW
13159	27060	A	13300	359	372	KKKKICGGKKNPPNKKKVKPRGEKTPLK

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						GV*PFFCLEGGFFSPHKFFFFFIFSPNIC SPKKSFFLKFPFPALFFFNLPFLKNIPSP PFLKKASF*EIFFCGPPPPFFFFQNTLF FFPPPPPPPPPPPPPPPPFLDKFAVY
13160	27061	A	13301	233	406	VTVEGMEEVLASSEGMSRPTS*V*FL KYL LGAVAHAKPSTLGRGRIT*AQE LKTSLCNKVRPRLYKINK
13161	27062	A	13302	92	429	GSHFNSELIEMKFYIIRNIFITLNCFY LIKHHQHFHYTKFLLVSVINKF*LATVAH AYNLNTLGGQGGRSA*THEFKTSLGNTV RSCLYKNLKMSSWWCTAIWEAEVRGLP
13162	27063	A	13303	302	140	GGAVNSVQSQAWWHMPVVPVWEAETGL LKPRSLSL*CPMIVHVNSHCTPAWAT
13163	27064	A	13304	115	312	LRSPSFVLSRLKCGGTIMVHCSFDLLG *RNPPALPSKVETIGLHHALLRLLI FF*KWVVLFF
13164	27065	A	13305	90	246	PGVVAHACNPSTLGRGRIT*GQEFKS SLCKIAPPPERKEGRKEGKKKRG
13165	27066	A	13306	19	310	DSSFSPIMCFGMSVNKTGLWLGGKKKKK KKKKGGPP*KKPLGGPNLPGGGKKKFFP *RGAKKNPPGDFWKKTLFLGGEKLGPPP PQK*NPFFGGGKIGPTPPPKIKPFGEKK KF
13166	27067	A	13307	179	56	WVLVYKKQSILG*AQWVMSVISALWEAE AGGSLVSTSLRIA
13167	27068	A	13308	425	290	KKNITLAPPGYFWPPQRFLLSPPPPNV VIFFFFLFFFLFFFLFFFLIQAEGIG VMRGRGEGKMGR*W*KFGRRVLNIRSI LLANFKHVVPYW
13168	27069	A	13309	214	371	IYF**RWISQAWWLMFPVPLKWEAEAGG *LEPMSLPGQYNETSPL
13169	27070	A	13310	975	572	AWGMVVGVGKHSLSVLGIEBCQASTALS LDKSGWEEAARREDVLCEDRRCLCHV PAGVRGSLKPELGSRKGNGQQSGSKPS VPSLGPRPQGPNGPALSKGTRPN*ALCF LCQTPADHSACKQAPHTLIPIR
13170	27071	A	13311	270	10	TPNKSIL*RLQFSNLIKLANLGLGTMHS CNLNTLGGQGARITSGEEFKTGLGNIDP IPIESKVIKFLAGMVSPDAVDAIKRTG TSG
13171	27072	A	13312	103	290	LTEVVSGLVIL*NCIYLLPQYTSTRVHAY IHTYIHTHTHTSGLSSTSVGSTNHKSKI FGGKKG
13172	27073	A	13313	136	1	SENTSSSLVTQAGGQWCELGSL*PLPPKF KRFSCLSLPSWDYRRL
13173	27074	A	13314	88	183	RVSTLLKKSCFFFFFFFFFFFFFFFFFFFF FFFFSSQKKKNLKNKKRE*KKSCFFFFF FFFFFFFFFFFFFFFFFFFF
13174	27075	A	13315	481	517	LLSP*RPKGKPKGKKRPNLKEKKIGEA RGGKERQRKTPORTGKQKKRRKYRIRGR RNYR
13175	27076	A	13316	307	196	GMHLYLPRTW*WVRVPIGSREIEVHAPL EPGSQRLVAEMTPMHSSLDNMNKSPPFP QPPKTEKQTKNPPKPHIA
13176	27077	A	13317	2	209	PARALDLKGPYMESCSDAQAGVQDSIY GDHL*LRAPAV**GQTVFVASPSKVGGI TGASHHPGLFFLF
13177	27078	A	13318	3	178	SFCFVSLREIIGQSLIMKTLP*ITHHT

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						HTHTHTHTHTQREIERERDRERGESQVLGC
13178	27079	A	13319	40	382	DSVPSLLLKLLMETGPHHVQASTTTPS *FFILEGFHHVAHAGLKLPPSSSRPPHLA SQSAGIYGCEPLRSARLIINYIGSRLWG LRNICLSQDHEECLLCFILQAISMYRFLG
13179	27080	A	13320	107	1	PPLIMANSQWAWLTPVVPVTLWEAKAGG *SEVRSS
13180	27081	A	13321	111	382	ASSQLLELAIQVFPGIWIPPTTKQKGV SGKTLVTSKIIAGLKMPKDSRSRPRTV HTYNSSTLRGQDRRIT*AEFKTSLGKI GRPCLF
13181	27082	A	13322	49	108	CGLY*FFF*ATRSWHVAQAGLEFLGLSS FPASASSVAGTTGMCCHHTQLHY*F*V
13182	27083	A	13323	1	257	ARGERERERERERERERERERERERE RERERERERERERERERERERERERE RERARERE*ECV*EGETVSDRERDFERA PVRVLGAVAIYIEVVCASLIQ
13183	27084	A	13324	1	248	EFQYILCSALIFGRSKILK*ATKEVKKS KHIPRISCQDTRKYNWSAKAKRRNTGT GRMRHLKIVYRRFRHGLHEENLFLKH
13184	27085	A	13326	375	1	PPKRRGKTHCSPKVPFPFPQNN*TTTTP QLIICYL*RGGVFFSLPLII*APPAFFF FFQFFFFFFFFFFFFFFFFLQGQYQFRDT DAEGHLASSRPSGAVFPSQGMHTTGSTR RWGQCVFPFPTRP
13185	27086	A	13327	382	15	NWPKNCPLHFQNWFLRKTQIFFCLKNF FFFFPKKVFYPPKKPFLEKPWPPVLN*K KPPPPFFFGWGGPGGQYCPFKKAPPLFI RGKERFPLWKGKDDFFQIPCPGPKKKK RAAADLGT
13186	27087	A	13328	2	220	GRVGSSRARAVALLFFFFFFFFCFFFFFF QNPLPKRGEKKKNTPLKKRPLRGGFK KQKEC*EKKKLSGPK
13187	27088	A	13329	427	289	IQLWSSL*K*LHTHTHTHTHTNTCFL TVMKELSTHPGNK
13188	27089	A	13330	203	269	INFGPPREPGGFNQKPQFPSAPGFEPWN PPQGPKP*KKKKRKKPFKVWAPGGGSKV QNPGLRETGVFG
13189	27090	A	13331	216	418	DVPVHYCRLYKPCTLRLLHSIYKKQILLW PGAVAHACNPTTLGGRGLWIT*GQEFEA SLANVVKPHLY
13190	27091	A	13332	160	325	WERQLFKIAQSGLARWLTPVIPALWEAE EGGLFEYTSR*LWATQQDPISKMFK
13191	27092	A	13333	339	62	GMLPLFVPPQKRGSPPYPCYGVNSPPL KKQRFSSSLGIVLPPIVFITPPPPAFF FFFCFFFFFFFFFFFFELI*RRLMRRRM FSCFLHCP
13192	27093	A	13334	45	384	DPSVRINTLLALLLIRITF*LPQLNGYI EKSTPYECGFDPIPARVPFSIKFFLGA ITFLFLDLEIALLLPLP*ALQTTNLPLI GMASLLLIILALSLAYE*LQKGLH*AE
13193	27094	A	13335	270	660	AGSRRPLRVPGFSLMMSPSLCRPVCVA QCIRVSFLITVGAVLRPGFQCLDWPCLV YARLSGWTGFPPCRYGKGCCRYDEGCC FEGGCCRCDDRCRCGEGCCRCDDGCC YDEG*CRCDGCGHYGE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13194	27095	A	13336	298	349	KTPFFYGLRGSKIGTL*CSGVIIAH*SLKLLGSSDPLSLVAQAARTTGACHHDQLTNAFFFFPLERVPTPLKNNPFLWVGKVKNWDL
13195	27096	A	13337	865	518	KSATMRMVEDTHKMPAWGGYSGSLQQERGELSSLP*PESPPPLLIIFLKLPSNPLPCSPLPCTQGGPQAPYVSIHTSLKFPNAKLSVCLSRATIEFS
13196	27097	A	13338	154	354	FNLVKPDGYFVLFIHILPTDSKSGKAPGAPCHSRNFHIRKTLGWVQWLPVILALWET*FSHQENSGLGAVAHTCNPSTLGNQGGWIA
13197	27098	A	13339	262	11	QHFHSRKLTP*KM*LSAHSSTHEAYVAFPKAHKPGLNSTAF*LGTEAHACNPNI LGGQGGQITRGQAFKTSANMAKPRLY
13198	27099	A	13340	358	164	TKKGKPRFFLKNSKISRWWWAPVISGPWECEGGAFFV*TGPRKIWLTEVGPLPFPNLGKKKENPF
13199	27100	A	13341	147	2	FRPQKVSVRVGVLAHACNPITLGAQGGHII*GQEF*ASMANMVKPSSC
13200	27101	A	13342	367	17	TSRSWNLFHVLVRFPPTADKDIREIGSFTKKRSLIDLTPYAWASTILMEGKKQVTSSSINGSRQKVRSSQSGELSLTPSDFSWAHWLMPVFPALW*SETGSLFEVVRPSRPAWPTW
13201	27102	A	13343	166	492	EGTOETLCGCIICLVRGDALNLFHLKCSWVGWRGAICCMELRETAKQLSVWKLYPEIVFSFSNNNPRPGAVAHICNPNTLGG*GCRIARAQEFETNLCNIVRPHLFR
13202	27103	A	13344	804	1124	TFFFCFFL*DRVVDVAPGWESSDMTMGPLQALTSWGSTDPTTLGLQSGLDLQDTWPPYPTSFYFFFLQGRGTLPLRLVLNSCTQAILPPQPGQRSKTPISLKTN
13203	27104	A	13345	280	448	GGGGKKKKTTPKPPLEKNFSPPP*FPPP KKQIKPPPP*GGGGKKKKTTPKPPLEKNFSPPPFKPRKGIFFLPPLSWVKKKGDPGGTRPLAPL
13204	27105	A	13346	232	400	AELLRYCSCGHFL*SMARYKTKPGVRWLTPIVIVFWEAEAR*LHEPRSSRPASATQ
13205	27106	A	13347	138	332	RAVVKPSFEIFYFFF*RAHTF**SCVCLCVCVCVCV*THTHTHTHKHTHDY
13206	27107	A	13348	314	395	WLGIVAHAYNPSTLGT*GGWIT*GPEV
13207	27108	A	13349	388	371	IMNGWQDKELVSRVIQTGIKK*KPRNRP EFRAPP*WHERNGRKRERMEGRKERER KKGKGERKRKKEACIYKVKIEISNNLANLIINVER*DRRRPDILSWVLSRVRSSVFIALVTCLTSPQFFLSLHLNQLFPLGKNL
13208	27109	A	13350	412	40	LVFRFWMCLFSRELFGCFSHLLTKSMSQM*VVAFGDIMYTFDLLFIKTKNNCKLWQGCKEESLIHCWRECKLVQPL*RPI*RS LKKLQMGLPYDPAISLLETYPKERKSVY*RNICTSGRVG
13209	27110	A	13351	372	148	FFFFFFFFFFFFFFFFFATGSCRVA*PGVKWLIISTVPLLIISTGVLTCSISDLGQPVHTSLGNLVVPYSQELPY
13210	27111	A	13352	209	206	KKKKKNFFSFHGKNPNGGPFPGPPPPPF*TFKKGGGLPKGPPPKGFFWNPPQNG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GGGP*PGGEKKT PKPSLGLV L F F F F K F F KKRPTAFFFLKKKIFF
13211	27112	A	13353	43	334	KKKKKKKKKKKKKKKKRGGGPFKISG GAQFFRGEKKFFFFFLGGGKKT PRGFEE KKPFFWGGNFWPPPQKNFPFGEKKKFL GGGGGKNRVFFWGEKIFSLGFFLKKFF* KKPEGKNFFPKKNPVFSPPPP*KFFFF PKGEIFLGGGPKIPPKKRFFFKKPPG GFFSPP*KKKKKFFLPPEKLGPPRNFK RPPPPFFFFFFFFFFF
13212	27113	A	13354	264	496	KPTILRVTHFLEGCEKEFLLPVAFSNF SEPLKRYYYWLGAEAHVCNPSTLEGRGG QIT*GQEFETSLVNMVTKCLY
13213	27114	A	13355	183	9	IRSPKIPEIRVFFFSRWSYALVAQGVQ WGNLS*MHPPRARFQPLSSLSVPST*KY R
13214	27115	A	13356	208	378	ETCLEFKIIDEMDKCGKLWLTGAHT*N PITLGGQGGQTT*GRAFETSLDIMEKRY L
13215	27116	A	13357	256	341	KGQTQWLTPVIPTLWEA*AGLLESRSS
13216	27117	A	13358	78	344	IVGLFESESKKGQHI VSGWIYLRLLIYR FLFPLFSLCLCKFFFFFSPETEFCEVPQ AGVQ*HNLG*LKPPPPQLKQFSCLTLP SWNYR
13217	27118	A	13359	259	291	AQ*LMPVVPALYEAEGSSLEPRSLLS VWAT
13218	27119	A	13360	448	121	RLFDLGNKKTSSFVQNSENAKYEDSLQF YCRIYIYVYIYVYICIHCVYM*TYMCM YICIMYTYTHVYTHVMCIHTYMCIA* YICVYIYIF*KACLPLAISTLSSGH
13219	27120	A	13361	125	262	FSFQASVEFTSKTVWSVWQWLTPPIISTT *EAQAGGSLEARNSRPD
13220	27121	A	13362	362	46	ARAKGPKKIGFSGKMGP*GAPPPKMGK KI*ITPPPKFLFFFLGKTKIKNPPWGF PFGFPKKKRGGGARR*KTPSPFREKPPP QKLKRFKTPFPPLFFFKNRP
13221	27122	A	13363	378	48	FKKAAREKVSTRKFRGFVCLFWDFFWRQ SHSVTQAGVQ*CDLNLHPPGSSDSPAAA SQVAWTTGTHHTQLIFIFICRNKISP SLLKKYKKNLPGVAVAGACNP SHLGG
13222	27123	A	13364	174	396	SLIFILEKRECYPRSLFTVANFTVAKR *QTLNCPSTDKWINKMCHIHTVEYSDI KRNEIPMRATCRQTLKA
13223	27124	A	13365	76	280	PLLPFKAWQVVGCHYV*KLD*INCYFR ALLAFSEYMYIYIYIRTHHT*YIYIY IYKLTYSHLKVG
13224	27125	A	13366	133	324	YLL*ILVYCSHLIFSLLCLEGIILWVFI IATLITLNTSHLLINIVPIAILDLAAGQ AAVGLALLVSKKKKKGPPLKKPPLGAQI SPANQRKKFPKPKPIKTRRGTF
13225	27126	A	13367	488	190	FSYAACFLPQC V F V C T F I Y L H A D G F L L L I I F F E N S V F I L C H S C W F C F L L Q W F L L M N L F S L F L L M L M H P V S * M E C S I Y S F S S L I I F H F S L M L L F F C F M I
13226	27127	A	13368	229	372	YYATKDFSRPRAVAHTCNPSTLGGGRGQ IT*GRQFETSLANVVKPOLY
13227	27128	A	13369	122	2	KEECVGS GTWVMPV I P A L * E A E G R G S L EPRSLRPAWTKK



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13228	27129	A	13370	43	412	RPTRPKRQNYGDSENISGCGGLGKKGMN GKSTEDFEGSETTLYDAITVGTCHNKFIRSHIVYNTKSGP*HKLWTWGGHDVSV*VPQLRKTYHPGERCL**GRLSMYRGREYIGNLCIFCSLLL
13229	27130	A	13371	136	1	KSPTWPGMAHTCNLSTLEGQGGWIT*GQGFETSLANMVKPSDAW
13230	27131	A	13372	228	385	GLLIHKLEFKHFWLGTVAHTCNPSTLGGQGRHIT*GQGFETSLANMAEPCLY
13231	27132	A	13373	277	429	LETTTKAGLEPTIIFTSSQMSIWFQNK PWDSSKLLFNLLSISSP**SSKNY*PWQSTVAHTCNPSTLGGQGRWIT*GQFEISLANMVKPARVGRHVIRGLQVS
13232	27133	A	13374	194	3	NQENYIYIYTHTHTYTHTYIYL*LLLQWVYLAYFLCLSYPSLFAQGFTHTTYTHTHMTLIL
13233	27134	A	13375	377	228	DRVLLLLPRLECRGIIMAHCRPLRLVSN S*APALSFQSAESTGVNPVS
13234	27135	A	13376	255	465	NAWKCPFIYKITFVIFLIHVSCKKFRNY RQREWKLPTRPLSPS*AIIFPVTCTYT SRWPEATKDPQKK
13235	27136	A	13377	336	38	VWCTPVVPATQEAEGSLESGLRLRQ*AVITLVNEHRESALASRRGPEETSSVK PELPTILAHTCFSLPRTGQDITSRFLAQ RNTENLELQMEARA
13236	27137	A	13378	376	293	FFFFFFFFFYFFFFK*KFLTCKKILSSQYI
13237	27138	A	13379	215	16	HLTWSFTTATEGSKTVTQHSVYRKAKLG LGAVTHTCNPSTLGGGRWIT*GQEYKG IPPHGLEDVQ
13238	27139	A	13380	184	64	VDESLEGWMMDEWMSGWRGGCINRYMHA WMDG*GDGWIGG
13239	27140	A	13381	233	417	LKPITKGRKPRGFFLPFKPKQKKYFWGF KKKKKKKKKKKKKKKKKASRAPF*KKG POKTP
13240	27141	A	13382	34	360	RWNTTNADHDLKDNILSPPQINLYIRON SSRLCRHH*QMSKSPVKIPAGFVLYI* IYRYTHTHTHTHTHDSELYMETHTRMA NTIVRKNSLEHSYYLMLRMTIKLP
13241	27142	A	13383	214	71	QTLNTDSGPGVVIHACNPSNLGGHGGKI I*GQGFETSLANMVKRCLY
13242	27143	A	13384	352	312	DKQLTLHRTDSLIFYTY*PPQSCPEIS YNNFPCLSQYLYLCPSLHTHTHTHTHTH THTHTHTHTHSVGRSLFFSGPHTE APRSRVSVYT
13243	27144	A	13385	393	271	IEGQIQYTSTIGNKFKDFYLILCKEGIM SREISPPSSCHLRQQ*RVRLRERDRERK RQRERQRE*GRSVLHPHVT
13244	27145	A	13386	180	440	PVEERTLCEDILCFPSVLLCIQPHLLI QHACFKYPNPNSRFGSWPVAHICNPS TLGGGGRWIT*NQEFEARLSNMVKPRLY KNI
13245	27146	A	13387	190	47	EGEKGVPSTILKMETLLGTVAYPCHPST LGGQGGRIAEAEQEF*DHLE
13246	27147	A	13388	188	470	ARPPCKGRDSSAEGPPGPPFSWSSLGC WTREPPGRGEPIQAVRREESAQDWARP ELIIKEWWPGLVAHTCNPSTLGGRGWI A*A*EFENSQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13247	27148	A	13389	454	367	NKKKKPPPRPF*PPPPPLGKTPFFKKKNP NPPRGGGNSPGSPSFGGKGKDPDPGGF FPPPPYPRGEGGNPFFKKKKKKRASLD P*WSSQPCPAYEKELNFAPVLATVTLPP GHSS
13248	27149	A	13390	34	354	HTLLALLLIITF*LPQLNGYIEKSTPY ECGFDPISPARVPFSIKFFLVAITFLLF ELEIALLLPLP*ALQTTNLP LIVMSSLL LIILALSLAYE*LQKGLD*TEY
13249	27150	A	13391	1089	792	THGFGPQVGSPLDLKQPKAMPGRGPSLG NPPPGCQQHSHGAGGP*VPPGPRQPVMA SRNLCPLALPRTTHPPSPGQTRDKPRTQ DRSCWRDPRNGPGV
13250	27151	A	13392	299	428	WIRCGRGRSCLPVPHSAPALLSPLVVD GTRRREAGGGTCQGGSGCMGAHWLGGG EGSGCRSQALPREAAEARREFKHGGIPR H*LTESLVSVEFRHA
13251	27152	A	13393	382	413	HGKTHLYKKFKNKKFKATMPA*WLTPI PTLQEAEEASLKPSSRPAAVVTWQDPS LQKI
13252	27153	A	13394	64	401	GGIPKEDSQAGFTGIGERQQGLVPIPL KNGQLSTDACVPPWGRVGVVERAGPPNQ AGEGGGQQEQCSLGLLPEANRCHPCNPS TLGGRSGQIA*GQEFELSLGNTVRSCPY
13253	27154	A	13395	146	18	FSPGVVAHACNPSTLGGQGGQIT*GQAF KTS LANTVKPKRPQ
13254	27155	A	13396	1056	679	DIQVPERPL*NVPEPEAKGEPDRAVGE HIDRDCRSDPAQQRKIFTNKCRAGCR QREMMKLTCECRSNFCIKHRHPLDHD SGEGHPTSRAGLAASRAQAVASTSTVP SPSQTMPSTSPSR
13255	27156	A	13397	440	423	IHSPTQRRV*QRERERERERERERERH ALAERNRTREGISGTTGERGNLMLVGGH LPGPLSSRRLGFCPDGFGGQHCLAQGDQ VRL
13256	27157	A	13398	2	256	IETLGSVEFIPYENTYQTYLKKKNRNS HMOSQPNRKGHIRLKYIAAWA*WLTPI PALWEAEAGRSLESRSRNPVSTKKKIQK
13257	27158	A	13399	102	922	LSFFLFSETGSCSVAQPEVQWCNHSSLQ P*TPGGPSMQFQLPQEQGQRTAVWHGGR A
13258	27159	A	13400	198	55	KDYSAVVHTCNPSTLGGGGGWIT*GQEL KTSQANMVKPHLYKNPKIEF
13259	27160	A	13401	19	447	ESALNLP SAGIIGVSHRTQPIFCILNAL ALGVLILERSPLQSPQVPPSHSTKPGS LPSVTGRGPRPRAAEPTAQGRYNSN PVLISPGSVHPASFALPAEPP*TGAPST PRPCVLRPLLLGNAMDLLCTKLSSRLPP YRT
13260	27161	A	13402	93	410	DSNLNYSLFFHGEADLGTNQLVTHPSTT AMYFEHYCQPP*IVHGTINT*PPVVKHN PIHIITPSPCLRASTAINLLSHINCYS *ATPHPLGYQQTYLPLTVHST
13261	27162	A	13403	55	387	SNSHTYSLKKSAGITKFNWHIVNCICI CQVVVPLEMVNRHTVILCQYPVKPRILY QHHTAILVTILTFTLRPGVVSHACNPST LGGQGRII*AQEFKISLGNIVRPCLY
13262	27163	A	13404	39	365	SGDRRVRLLLKIITF*LSQLNGYIEKST

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						RYECGFDPISPARVPFSLKFFLAITFL LFDLEIALLLPLP*ALQTNLPLIGMSS LLLIILALSLAYE*LQKGLD*AE
13263	27164	A	13405	32	350	HEFATSTSEMTKGT*IVKRRIKHTLC RRCGSKAYHLQKSTCGKCGYPKRKRKY NWSATAKRRNTTGTGRMRHLKIVYRRFR HGFREGTTTPKPKRAVAASSSS
13264	27165	A	13406	326	668	LQFKIFCMPGIFTTISEVSSMSN*RTAYG SQSFHKIVLI*LATFGQALSC*IL*IHL CYLKNKTKHRALVAHACNPNTLGSPPGR IA*QGEFETSLGSIIVRLLLSTKNLKKKK NM
13265	27166	A	13407	170	472	KLISVWSEESSYCVHEGPEVVPQKEYS WLEIGKAEMERSTLESLLGATLEALSSN PTRKMQLGLKLKLQASAFKEEPWLGVA HACNPSTLGG*GGRIA
13266	27167	A	13408	178	422	FYNRYF*YTKYQNTENIVCKIMSFRLV *KI*SLPGAMAHACNPSTLGGRRGRII* GREFETRNS
13267	27168	A	13409	274	444	LFSQYIVFVHYSSFVLILFV**LFSQYI VFVHYSSFVLILFVILHNYTYIYIHTHT HTYTLIFLLIFSQISLGMKLIL
13268	27169	A	13410	205	23	KEFLKFHRKCICQOVKKTWPRAVAHACN BSTLGGQGKRIT*GQELTSLANVEKPH FSNS
13269	27170	A	13411	25	426	SVWWSLETRSSRLRLKKI*NLQNKRR KFEHRHAQRKYDLETQGEDAIYKLRER RKEEE*EKEKKRRRRRKEKEKKKKPTL LCLKKQRNQHLDLRLPASRTVKKLISVV *ATHSVVPCYGSPSKLIQSIH
13270	27171	A	13412	227	52	EIGSHSCHPGWSTVAQS*LTLSNS*TQ LILPPQPPRELHYNCPVPCPAFCRQAL MF
13271	27172	A	13413	345	67	SKCCYVVAHDCILLDLICLYFLELVGCV DCFSSSLGHY*PLFV*IFFLSPSLLEWY SHYEHICVPHFSKAPFIPLHFFPSPEFP FLCIEMVYV
13272	27173	A	13414	345	33	KVFFFLIICKMRMKNQKNKHGICLLNS AMNTCISFPLRQIMTWWLEVTQIWGV LFYLFHFHFIEMGSCPGWSAVA*SQPSATP VWSQVILLPQPPEDLGNS
13273	27174	A	13415	187	415	FNQGWAFLEFFCVIFSYPWKDRNRITFS IKITSFQESVLKLFCEFEVS*ILKIGLG QVRWLTPVIPALRRRQADH
13274	27175	A	13416	143	50	CMKLQSSIVMLGVVAHACNPSTLGGQGG WIT*GQGGWIT
13275	27176	A	13417	170	17	KQMRKEGNGLLTISKVWKQPKSPSQS* *IKKM*YICTMECYSALRPEFPE
13276	27177	A	13418	7	163	IK*IWYI*TMYYSAMKRKKIMSSAAIW MKLEAILGEVMQEWKTNLMFSFISGS
13277	27178	A	13419	901	709	SGRKTSLGNIARSCLYTKSFKIHCPLPV PATQAEAGGSLKPRSLRLQ*ARSHHCS PVWVTTRP
13278	27179	A	13420	236	4	VIRAKTGSNSLFPFHTFFQGNLCFF QKKKKKKIYIQSKPGAMAHACNPSTLGG QIT*DQEFETSLATMVKNPLY
13279	27180	A	13421	46	141	NSVISAHCNLCPLGSSDSPSSASRVAGI TGWC*HCNLCPLGSSDSPSSASRVAGIT

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						GWC
13280	27181	A	13422	604	1121	LGSGDLP*EINPLSSCSLLREKDPPTTS GPQTDQPKKHLTNFKSAPYKTITDAELR VTLTVEAHLHPGEINSHVAHTKPVWWSL HTDAHEIWCRRSDLLVPTLPLIPLEAA LRNITHSLSI PPPKNFRPNTSTLFCVI FLINIRROEQYQASEPKPSHRIPCDLHVY AQMA
13281	27182	A	13423	214	22	IRESSSTPSSPTLPESCNSIPFPF*KFI WSGVVAHAYNLNTLGG*GRKIARAQEFB NSTRAGLW
13282	27183	A	13424	397	330	SEYNSECS*VQWHTLVVSATQEAEAGS LEARSSRLCALIIPVNCHCTPAWAFPM
13283	27184	A	13425	729	885	AKCYPVRNLSLWPGAVAHACNPSTLGGQ GGRIT*GOEFRTSLANMVKPHLY
13284	27185	A	13426	231	2	ASVFFKATLVDLHW*YIYTYIYTYIHI YTHYTHYIYIYIYIYIYIYIYIYIYIYI HINANQQGYIYTGRTPICFF
13285	27186	A	13427	184	171	LS*YIYIYTHYTHYTHYTHYIYIYIYIY QFSSQSS
13286	27187	A	13428	372	166	CKFRPRKINTTFSHICGS*KVDIIEAA* HWLGTVAHACNPSTLGGQGRWTI*VWFE KASLANLLTPLLQ
13287	27188	A	13429	391	437	MYSLGVGFFHSTI*LLKDIWFGVVAHT CNPSTL*GQDGRIT*GRKLETRPGNRAK LYLYKKNSN
13288	27189	A	13430	39	254	EFIPRAQDLETSQGNVRPRLYRKFKNN *VWWCASVVPAMWEAEAGGLSEPGRLRL HSNMDNGERSCLKKK
13289	27190	A	13431	336	488	DIWPGMVAHACNPSTLGGQGGRIA*A*E FETSLSNMARPWLKKKLARHSGA
13290	27191	A	13432	154	481	FFFFFFFFQKNGFFF*KGIFFFFKLEGR GAIFV*PNLTLP*GKSPASPL*KGGKK GGAPPP*LIFFFLKKKLPLLGQGLKL RALGKPPPFPSQGGINGVKTTPFGL
13291	27192	A	13433	388	280	KSKLKGCCVALCLGLI*SVLLA*PKT *LFCVSLDMYIDTTCSLISISYLSIYLS IYLSIYLSIV*SVS
13292	27193	A	13434	187	48	SISSTKGPAGAVAHAYNPNTWGGGGGRIT *GQEFETSLANMVKPRNS
13293	27194	A	13435	71	309	DSVSEEEEEEEVELAHPLAERYHCERA ET*VKALLWLELCDERVSSRSHTEDCT EELFDLHARDHCVDHKLFSNLK
13294	27195	A	13436	18	375	RPAVPGRPTRPINTLLGLLIIITF*LP QLSGYIEKSTPYECGFDPIPARVPFSI KFCLLAMTFLFDLEIALLLPLP*ALQT TNLPLIVMASLLLLIIILALSLAYE*LQK GLD*AE
13295	27196	A	13437	373	27	THPYYSHQEQSP*PLTGALSALLMTSG LAM*FHFHSITLLILGLLNTLTLYQ*W RDVTRESTYQGHHTPPVQKGLRYGIILF ITSEVFFAGFF*AFDHSSLAPTPQLGG HWPPTGITPLNPLEVPLNNTSVLLASGV SIT*AHDP
13296	27197	A	13438	575	699	LGTVAHTCNSSSLGGRGGWIT*GQEFET SLANMVKTCPOKK
13297	27198	A	13439	247	168	LENLIYTRVLERHREAKVHFPFSNISYS DKRTDTFVLTKTH*HTHTHTHTHTHT

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						HTRGSHFFY*HTHTHTHTHTHTHTTRGSHFFY
13298	27199	A	13440	391	168	TKKKKHPSPRGAREVFF*QPPPPFCVL*FFIVFFLSQGGGGGGGEFFPPFPPTSPPPPPRGVWKKTPPFS
13299	27200	A	13441	403	246	LFPTAIIGGPPGFPPPPF*NPAPefffwGPKKKKLSPPPAIKMVFFKGPPP
13300	27201	A	13442	305	414	KNNFHPSTLGG*GGWIT*GQALETTSLGNMVKPHIY
13301	27202	A	13443	269	409	PGTVAHAYNLSTLEG*GTMITQGQEF*I SLVNTVIPHLYQKKKKGR
13302	27203	A	13444	295	37	DPSYLAWHMVTPHQVSTQHTLPRPRPCLPEMNFLVSLKIWCWPGTVAHACNPSTLRGRGGWIT*GQEFETSLANMTKTRTRGSAR
13303	27204	A	13445	256	388	FCGFWPGAEAHACCPCTLGGRGGWIT*GQKERTSLAHMVKPRVC
13304	27205	A	13446	277	374	SRLTATSSRGGWIT*GQEFVTTLANMVKPLLY
13305	27206	A	13447	14	387	PQVIHSPWPPKVLGLQA*TTSQAWLTPVIPALWEAKANGSLEVRSS
13306	27207	A	13448	185	379	HFGRPRPADHLRPGATNHPGPQGETPSLL*NTKKKKRGRPFKKKKLQSLVWQNKIFFLAELKLLW
13307	27208	A	13449	168	346	ISILRTNMISIKINLRLFIDELKKRDPFIFPYFFFFFFFFFGGNHSL*SLIVIFLIC
13308	27209	A	13450	57	176	VAESRPGPGGTATELVPPSTRLLTRAPRDLLTGKRKPPPLGRMSRARVQWHNHF*TESCSVAQARVQQRNLGSL*TLPPKIKQFSCLSLLSSWEDCLSQRVRDCSEK
13309	27210	A	13451	411	241	PPLFFFFFFFFKQFSPV*GGGQGWDFGSLQPPPPRVKQIFCPKIPPPWPPKGGVPG
13310	27211	A	13452	307	298	PTHSIVRNKSL*IN*TSSMCSGLKVMRR*SQKQEDP*SGVVAHACNLSTLGRRGWIT*GQEFSTFLCPSA
13311	27212	A	13454	191	108	GWSQTPGLGRSSLLSLPQWWDYRMQCRGVILAPHCGLDLLGSGDPPASASQVAGTA AFENCATSFWLP*FLNTQCFKIYKTKN
13312	27213	A	13455	242	400	IATLLDYLQIPNTGPGAVAHACNPSTLGGQGRWII*GQEFENSLANTVKSCL
13313	27214	A	13456	1	346	YVTTARCSCWAGTESHMGAKDFYRQEKHPFHADSGIGWA*DRLRQRYGRFGRM*F SWARGAGEKHSLS*AQWLMPVVTTFWEVKEGRSLEPRSLRPAAWATWRNVSTKIKKKKKG
13314	27215	A	13457	166	289	VRSSKLNWVRWLVIILTLWEA*AGGFLEPRISRLVWATQ
13315	27216	A	13458	220	76	TASLKLKSWLDVVAHACNPSTLGGPGRWIT*GQEIKTSLANMVKPSP
13316	27217	A	13459	219	46	SPPLKKKNFFPPGVMCAPPRFFLKGPPQNFFFFFFFFFFFFFFFFFLKQ*EQTFLLIY
13317	27218	A	13460	126	1	VVSLGAVARSCSPSTLGVQGG*IT*SQEFETSLANMVRTLTS
13318	27219	A	13461	330	420	NICSWAQWLTPTVPAL*EAEAGGSPEVTSS

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13319	27220	A	13462	577	766	AQWHTSIVLAA*EAAAAGLLEPRS*SRLKCTMIIPINSHCTPAWQHMRPCLLKKNFSNSFISK
13320	27221	A	13463	206	387	VTVGETEAEAGRGHLLTCCVLKTQKWLGTVAHAYNPSTLGG*GGRIT*DQEFETSFLGS
13321	27222	A	13464	167	41	DFWLGAVTHACNPNSVGG*GGQIT*GQEFETSLANMVKPWNS
13322	27223	A	13465	480	79	SRVISPLILNSVISAKSLLPVGSQGKS KGQVWSTQEERLEPGVMGEFTPGPCCLVSQGPSLCPSPPPYSFRWSRLSQAPGSI RVLI*RPAAATSAPPAQLGLPDTAFPP PLLSRDQQAAGRQDRDKGLP
13323	27224	A	13466	3	373	DAWVAHASAHASVCLTIDTLLALLLIITF*LPQLNGYIEESTPYECGLEPISPAR VPLYIKFFLVAITFLLLDLRLALLPLP*ALLTTNLPILVMSLLLIITLALSLGYE*LRKGLD*AE
13324	27225	A	13467	214	55	TRQKIFNLFSS*KKFLIPPARAKDFLFFIFFFFFFFFFFFFFFFSCSRILLHR
13325	27226	A	13468	111	358	VMKVFI*IGELVTQAYIFVKSHQIAHILFHSMYVLP*IKMFWPGTVAYTYNPSTLGGHRRIS*AQEFETSLGNIVSPHLY
13326	27227	A	13469	199	607	RIRGTSQKLLLLLKLISLIPKSQPTRGTP*TTFPPTNTNFPNPPVAATADPSPA HFVSSPYNPDLGSP*PECPSGRLQREIEQCKKDIONFPPTTSRICSNDSLKGSASRRRGHLFCERPVNQFRSPKPKK
13327	27228	A	13470	128	256	EDWMWWLTPVIPTPQEVVRSLEPRSS ELQ*AVIVPCTPSE
13328	27229	A	13471	94	388	KGEGKTEELWSWRSHRGTHLCLLADISALPLHYYYYYYFWQRWSLPDQPGQHGETPCLPKIQIINRAYWHVPVPTDQEADAR*LPEPNRQRSORPE
13329	27230	A	13472	359	73	ATEPGQLFYF*EESHNVQTAGVQWLDH GSLQPPTPLKPSFPLIHTGITAASHYT WLNQLLPMNVSLTTFYESPQLKIQRSHILCNSIHKFLE
13330	27231	A	13473	332	10	ILSKRGFPKPGRYCEVNPFLCVQGAK*VRP*EDTSLHCEIYHTHTHTHTHTHTNLKP*TSKELIPQKTESLFFSLCIKKSLLRFQTFPDAGSTGNSVGCACFISK
13331	27232	A	13474	355	385	IMVCIQSCVH*KNN*FWPGTVARVCNPRTLGGQDRQTA*AQELKTSLDNMAKPCLYKKFF
13332	27233	A	13475	297	425	RKSAWWLMPVVSPL*EAEAGGFLEPGSLRSAWATWGDPHLYKK
13333	27234	A	13476	160	1	KSTGRLGMVAHICIPSTLGSQGGWIA*AQEFETSLGKILSLPEIQKSASLITW
13334	27235	A	13477	334	79	GMKEQINFLYQKRGIKPNKLQAEENVVLIHYN*KLLSNSFK*LQDTAST*YFFGNLYNRPGMVAHACNPSTLGGRGWIT*GQEF L
13335	27236	A	13478	234	385	YAKFHVSINEKKPDVAHACNPGLTGGQGKNIT*GQEFKTSANMTKPRIY
13336	27237	A	13479	408	129	KRSINRKKGGELSSSHFLLLLPPLDEE PPSPPFCPLPPFPFPCPLPQSG*GACGR LHPC*MDLGPCKCPARKVFSHLSCSL

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						VLQVCRSP
13337	27238	A	13480	251	384	TITPWRGAVAHVCNPSTLGGQSRQMT*GQEFKTSLSNMVKPRLY
13338	27239	A	13481	164	300	AGDDSDNSMGLLGRIHEIKFFKCLGPCM TTKFIVPALWEAEVGGWLEPTSLRLR*ALIALLQCTPA*GTVYDYKVYRPSTLGSRRMA
13339	27240	A	13482	2	30	TGCHQFRFLNNPFSHPHVLQLVSPGPDCLIFRYFKF*LHQLM*INPNANFCGARSFLCKFRVWIS*LRYPVALSVLFVK*S VQI*VKKKKKKKKKKKKKKKKKKKK
13340	27241	A	13483	39	199	LDVGTCSPIVPASQEAAGRLHEPTSLRLW*AMIVQLYYSLGDRARPCLYLKK
13341	27242	A	13484	18	72	TRTRSYPGSTGCQLHTFGLVSLYNCSQFLITNLYISITYRDIY*YIYIYLYREIYLYIYIEIYTYIERVYIHI*ILGLQVANC IPLD
13342	27243	A	13485	266	496	LDSASDITQAGVQWCNHSFL*PQTPLK*ASTSAS*VAEITGLSQHVWVKIIMSVSLSSYTFIQLEPSILLYGNTAP
13343	27244	A	13486	286	72	HILSHCTVLWFLTPHHGTHYKNTTGQPSIVAHATHNLSTLGG*GRWTT*GQEFKTS LANTVKCSDAWVDRD
13344	27245	A	13487	309	6	RFFFFFFPGKKGVFFQRFFFGFPRGFPPRFFKTGPEIFFFGPLKKKKNFPPGGKIVFF*RGAPPPPPPPPPFLFFFFFFLKNYLLLEKVQSPEKEG
13345	27246	A	13488	183	459	RRVKKICKCIIWQNNYL*KGINICSMPOKKKKKKKKKKKKGAPFKKKKKKIS*GGGPPF*KTKIKPPGGRGFFFFFGEKIM LFPVFI
13346	27247	A	13489	348	1	CEGKDGLP IQFASWFKYAGFHSLESIFQSF CQTKKLEAPKELSPCSQLYRYNWQLTCRRMKLDPHLLPYTKINSRPGAAHA*N PSTLGG*GGWII*GQEFETSLTNMGETP PTRP
13347	27248	A	13490	313	320	KQGGPPLAQARVQWYNLSSGETSLPLPGSSNPPPSATGVAGTTGSPPLA*LIFFFL*DRENGDQRKL
13348	27249	A	13491	187	350	GNPVKK*IKNTSSSGWVWMLPIIPALWDAEVGGLLEPRSLRPWATERDSVS
13349	27250	A	13492	211	83	EYAKKNGKLLSWRKYL*SVVCVCVCTTCVCVCVCVTTCIKNI
13350	27251	A	13493	286	407	LGVEAYACNLNTLGG*GGRIT*GQEFETGLGNTARPCLYF
13351	27252	A	13494	897	1033	KFIFKQMQWDDHSSLQP*TPELKQSSCLRLPSTWDYRREPLHLAM
13352	27253	A	13495	265	3	HLILLEEELTWQRGKWLKGRVSLCSLGS*TSLSLTVLKKGRGLGVAVAPSTLGGGRWVALAQELETS LGNMVKLSLSKIQKLAGMV
13353	27254	A	13496	319	1	CFKLWDTCAQCAGLLHRYTCVMVVCYTHHPEFCYNIMGLPKYMWSYLWPKCCHAVYHFRYIKNLLPGCVAHACNPSTLGGRGWIT*GKEFKRRMKT*IGIYFI
13354	27255	A	13497	265	11	VLGEVSNQHLGAPSNRTPSEVPLAQAAQGRPSLVPPSAIVFPSTICYAFLSISMPIIP*VWEAEVGELLEPRSLRQA*ATW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13355	27256	A	13498	164	22	GIKRRKLIKSGVVAHARNSSSLAGRGGWL T*GQEFETSLAKMMEIPSV
13356	27257	A	13499	277	363	TYLCYIFNCLFVGEIEKQR*LI*FHRS TLNGHILYVRPVPSPNPSQAVASPVTCTY MPTWPEVVESQKK
13357	27258	A	13500	1	270	YTCSVLLLVTVNLLCLLIYKLNFTIIGML RKKTVYIYIERIQYYLKQASTGCLGVY PTV*PYMYTTYMYMYMYIYIYIYIIL CLCLDG
13358	27259	A	13501	170	383	ILYSSKLTYPSPQIVIFFCGKST*GWVW WMPVIPAI*EAEVGGSESTSLGQAWA TGRKAFFVYKEYKN
13359	27260	A	13502	31	402	GDYLYLREGWQEPARREQAQNLEPNRT FPHLICTNYRFLSLAWSECEERNET TDKNQTVKDLALDMKRVLPFS*GHQKVI KVGVVAYACNPSTLGGQGQWITRGREFK TSLINMAKPYLY
13360	27261	A	13503	232	446	RNRPGAVAHACNPSTFRGRGGRIMRLGD *RS
13361	27262	A	13504	196	390	VNKAEEKHLYFVARKEILRPGVVVHTCN PSTLGGRGGWII*GQEFETSLPLPKTQK LAECGRGCL
13362	27263	A	13505	146	7	LKYVLYWLGAMAYTCNTSTLGGQGQWIS *GQEFETSLANMVKPCLF
13363	27264	A	13506	177	18	SONFGRPRQDHFRLDGRHSETPSLQEK VKKLTRHGGACVQSOLLERLRREDHLGP GGGGCSVP*SVNII
13364	27265	A	13507	117	338	NKILKKKKGGGRFKESKFTSPGLQGNST FMGPPKLNLRAGV*QRRGKNLGVPLK PFEANPLFARGPNTKNP
13365	27266	A	13508	306	443	LARYEPAVRTRAC*AQWLTAVIPVL*EA EAGGPLEARNLRPAWAT
13366	27267	A	13509	146	390	KMFKGHEQAHRKKKKRGGGRFKGSKFTS ACLQRNIFFLGPPKLNLRAGV*QRGDWK NPGVTQFNRFENPLFARGPNTQKP
13367	27268	A	13510	119	356	NEDRNLRGGCPGR*LLRTEGVCSNPAGW SGIRWCEESGGLFWRVVRGTESVLFSGL FVCCVFAQEKAKATGRAEVSCLP
13368	27269	A	13511	221	21	EDLQDKPLGSCYSTCGWAEQWYLQHPG GAGSKCRIWLGAVAHAYNPSTLGGQGRW IT*GQEFLSL
13369	27270	A	13512	163	418	TFPDDQCLMLQDHACVKRSIQSA*YLTP AVLAHWEAEAGLLEPTSLRPAWAT
13370	27271	A	13513	239	21	FGNLGGPGGRTACIQFSLGNIVRPYFYK TKPKPKPNQNTKIS*AWWCMPIVPATR KAEVGESLEPRRSRLQ
13371	27272	A	13514	135	11	KFFFWPGLAHAYNPSSLGAQGGRIT*G QEYETSLANMVKS
13372	27273	A	13515	162	57	BGTLRSRRPPLGGWVT*GQEFETSPANM VKRCLY
13373	27274	A	13516	424	54	PKRGFFPTPFIWVPPVFLPPFFKPPPR IFFLGGPPKKKFFSPPPGKLIFF*KGPP PFFFFFFFLEFFFKKKKRLGGFFFFFF FWARPFSFLSLFFFKETIPLYNIWMHK DSCKAVIHVYH
13374	27275	A	13517	310	349	GGGPLKKKLFSSRGGERFFFF*GAPPPF FFFFL*SSKIFIFFLKSFLLLLLLLLL FFFFFSQILFFISSPCFVFFFLNYTSRT



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						CSYVCALILPKGNTYSRKARHILW
13375	27276	A	13518	273	393	IKCLSYRKKATTLGGQGRWIT*SQEFET SLSNM*KPQLY
13376	27277	A	13519	450	139	IPPIALVSPFAKHTWQQMGLVRRSSKG NNMSKGWEIIHPSRIFCSNHTLLRIALW LGAVVHTCNPSTLVGRGGWIT*GWEFKP SKTSMERFCILSRHKRTRGS
13377	27278	A	13520	47	427	KMKQLFEMLVFQNWITIFLSHSIFRTIR* LTLEPLMFRYYFKQ*RTLLPPKF*DRVW LCHAGGCL*CSGTVSAHCNLRLLGSSDP STSAS*VAGTVGAGHHIWLILNNRELPK QKFFINSSRNLFET
13378	27279	A	13521	199	98	SLPSVKLSICCEFPEDIVSKDPIPVVLP VVKRESCLCALPNLLPK*EKTNIQVP* VFQSTIKAKAQLGMVAHACNPSTLGGRG GWIT*GLR
13379	27280	A	13522	314	18	QTLNFYILKIYNIISLVHC*IFEARFQI LV*V**NYPF*SLICFTFSWHETQNT** KNLIIWAGAVAHTCNCNTLGDQGRRIAL AQEIEPSLGNIAIQ
13380	27281	A	13523	18	231	CPPAVFGTSIEQIQKDYDKD*KIGQAW WCAPVPGTQAEVGGSLERSSRL*CAM STSMNRHCVPAWAT
13381	27282	A	13524	239	465	RVQVSECLHREKCLYFQLGLS*LIPQT GWLKQQKLPGTVAHTCNPGLRGRGKRI T*GQEFETSLANIVKPRLY
13382	27283	A	13525	388	468	SLRLGTVAHTCNPSTLGG*GGWITRSG
13383	27284	A	13526	342	369	CTLNTLLYSISDFGVSAPLATGGDITR NKVRKT*LRLGTVAHTYNPNTLGGQGRR LT*AQEFKNSLSNIGRPHLYKTKTKKT
13384	27285	A	13527	241	231	EYVCIWSHSSLYFSSSLYIHM*VCVCVY IYVHTNSHIYTHMYIHTHTHTHICIKL EEKYKEL
13385	27286	A	13528	241	231	EYVCIWSHSSLYFSSSLYIHM*VCVCVY IYVHTNSHIYTHMYIHTHTHTHICIKL EEKYKEL
13386	27287	A	13529	34	299	SAPASASPWGIGVLYRPLACPEDRFSPG PEANCGEIETTELRLVTLSPRLECSGTIT APCSLDLQGSRDPPPSAS*VSETTGASH HAQL
13387	27288	A	13530	158	45	SGHRSRARWL*PVISALWEASAGGSPEI KSLRNRRPG
13388	27289	A	13531	342	1	CFFLKGAPPPFFFFYFFNFFFLVGTID KLILKV'TWKWGPKIDKAVPKNNQARG LP*PDIKIFYKVWLGAVANAYNPSNLGG *GGWIA*E*EFETSLANMTKPQYKYYK LA
13389	27290	A	13532	589	742	RIMKMLRIKICGTGPGMVAHAVNPSSLG DGWIT*DQEFKASLANMIKPHLY
13390	27291	A	13533	74	446	HVGIPSRILTSVSHPRCHKHPRTESEHVV CAIEARHYQCKVSRPSDAAGSEGRPRDM TQDTEVADTPPPNISSITATRTMATIGV GVVAHAYNPNTLGGQGRRIA*AQEFKTS LGNLAKPCLYKH
13391	27292	A	13534	1941	1040	AFHLLPYLSSGFYCSLGPCFGLGSSHMA AWHKEPLHNACSDSRRSAPIRQGLGSPS ATHDTHTRTLAHICKEIFKERLHEIKER EIDS*RG*NTQR*VEREEAENKYKPTET

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						NTEIENHKQQEMLRHAGEERENSPREAE RKCNEKCEIKSRNSRKEARLRKKVKFK TNEKGKG*QIITVHKEKREVGRRERGRQ NKKRTKSTQHVTQKGDNR*SVKEEPLLR RAKRNSNKMKNERYVLRQDTHDSCQEKE KMRQRHTRKKLARETWKQVRHTLNREQR AKPRKKETKEIHIHSAILKC
13392	27293	A	13535	1192	1476	EIKRKWGPASCHACNPITGRPRRDHL RSGVQGPQGRGETPSLLKNIQISAWAW CAPVI*EIKRKWGPASCHACNPITGRP RRVDHLRSGVQGPQGRGETPSLLKNIQ ISAWAWCAPVIPATWEAEAGGSLETGSG GCTEPRSHHCTQAWVTE
13393	27294	A	13536	55	132	RAESCSLAEDGVQ*GNLSSLQPPPPK
13394	27295	A	13537	7	325	SPVEFRLGEPTKGTSSFGKRRNKTHLTC RRCGSKAYHLQKSTCGK*GYPAKRKRKY NWSAKAKRRNTTGTGRMRHLKIVRTFK HGFREGTTPPKRAAASSS
13395	27296	A	13538	259	274	KFEAAVCYHCTTSL*CHTVCFLSFFL LEIGYHYITQAQSGAMIAHCSLKLGGSS NPPVPAF*VAETRSACYNAWLVFKFLM GL*ELWKDMS
13396	27297	A	13539	3	68	QASVLPQKQLMSWQKLESTFVKFVNLV KTGRLGEEISCCLVVREYYSISDCLATI KLPASHLSMRKPRHKDFKSTFLISTKNQ GNHGHGTKGNEVNNFQQRISV*KTYFKK YNMRPGAVAHTCNPSTLGG*DWIT*GK NCQNQLS
13397	27298	A	13540	268	468	YRRLISKKFFKRWKSVSFFKFSFFWL EVAHACNPSTLGGQGGKIA*AQEFLLSL GNIVGPCLYKK
13398	27299	A	13541	308	437	FSWAFETIGSQAQEVQWHDHLSL*PLPPRF KRFSHLSLPSSWDYR
13399	27300	A	13542	7	244	AKTAPLFF*FETVSCFVAQARGQWHD SLQPRPPPGQETSMIKTSSDPPPPASQVA GATGMGHHQAQKI*FLVETGSPHVSQGG ALLK
13400	27301	A	13543	50	175	ALPAHTAVGQCSVEGFCVLSDEGDGA ARMKLVFLMKLSHETVTIELKNGTQVH GTITGVDVSMNTHLKAVKMTLKNREPVO LETLSILGNNIRYFILPDSLPLDILLAD AEPNVKSMNREAVAG*R*G*AREIFDEI ES
13401	27302	A	13544	47	362	VAFQGLQVPATNPANFFFFWKGFFFPV QGGRGGEKIGLRDPWPPGVRKIPGPTLS GTREKGA PPPPIYF*FFWKGGQKGGP GGF*TWDPKGPPSPTPPKGGD
13402	27303	A	13545	97	351	NKKKKGPPPPFF*KKRVGKKKKKGARAGG PPPKPPPGGPRGGPRGQNSKTPRPKG GNPPFKKKKKRNIFPAGPMGLKGGHGL
13403	27304	A	13546	214	32	NYIKISSVDGGAKIK*WT*NLKCLVLSV KNITRWVDCSSGVQDQPGQHGETPSLL KTRKTSWA*WRLGLIQRWRKMPWPSR
13404	27305	A	13547	350	159	QTGTLQKTKQKKQAQWLMTVILGL*EA KAGGLLEPKSLRPATWQDPIYKKKFF LERKTWR
13405	27306	A	13548	367	149	FFFFFFFF*TGSHYVAQNWTQIPGLNLP ASASQVTATTGMHHHTRHTPFPSLTST

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						QSVSTASWTYLQNSGRH
13406	27307	A	13549	321	2	GLVKVTHHGVDRLNLGYPSQASVLSFFY TA*MVQ*LQLPDKVQIYPAHPLFINDMP P*WLLKIPSFPGPTVAHPYNPNTLGGRG RRTTRDREFETSLANVVKPHLH
13407	27308	A	13550	216	13	GYSGETVFSMRKQQSGPCLQGPSPIM GKAGINQIIPKTTLGGRGWIA*GQEFK TSLANTVKPCLY
13408	27309	A	13551	199	391	KDFSIFTACFKRPFITGSQQEQWLIFP HAYNPSILGGRGRQIT*GQEFLLPARLG NMVKPCLY
13409	27310	A	13552	70	239	ATCVKN*RTSWAWWCVPVVPATHEAAAG GLLEPRSSRLQCSVIASVERHRTSVWTT
13410	27311	A	13553	105	257	GQAQWLMVPVLPALWEAEAGGSFAPRSLR LA*ATVPGPNFLKRAFHSLLNLFPL
13411	27312	A	13554	499	165	Y*MESHFVTQGGQLQWCSLGLSQAPPPEV GGWLELGRQRLPMKPKIPIWTPSPG
13412	27313	A	13555	415	719	YTDKSIRSISLLPVKGSHTSMCPVKFIQ LQEAGGIHMAKLSGQRVDREWRLGTVAH TCNRSHLEGKGGQIT*QVFKTSLGNMA KSCLCCKYQKLSWIWQH
13413	27314	A	13556	224	523	DKVSLCHPGWECEGWVQSQLTASISQG* TILFPQSPE
13414	27315	A	13558	355	1	QVSLQLPYCVLQFQHIYNKQAALLQRCY VSATNLLINAIWQYVNSLKMCEENQNV LQNMPF*HRNYFGEAGHGGSC*SQLLG RLRH*NCLNLGGGGCSELRLRHCTPAWA TKASPS
13415	27316	A	13559	73	259	KYVPHKGKISERRLCVAQAGVQWCDHG SRSLEVLGSNDLLASAS*VAGITGCWGS SDPHTT
13416	27317	A	13560	205	21	VVKISEDFLGDAKKWAYQEDIKRLRLG RGAVSHTCNPSTWRGRGWIT*DQEFET SLPKC
13417	27318	A	13561	254	481	LMALLPGSSDVLSEYGWEHFNVLIS KEIFILLFF*DGVSHELLPRLECSGMISA YCHLCLOGSSDRRDLKKQ
13418	27319	A	13562	174	369	TFFSPSMFVEPGPYIAQAGVRWLFTGA IIVHCSLKLALSDSPTSAS*VTATTGM PPLAFTVK
13419	27320	A	13563	371	109	LFSKAGRCILQNLCCMVSGKCWPMNGI DVTREYPTFAHRVLTAAATSGSDFLGQ AQWLMVPVPAI*EANAGESLEPKSLRLA *ATVPGPRSLSQLLLHSELCLGL
13420	27321	A	13564	206	486	RQLAAVHILVTPDPDHTWANYVTSLSL LSSSENGVNNDNTHFIGLLLRDYK*GWV *WLTPVIPALWEAKVGRIARGQELNSL GSKARPRFV
13421	27322	A	13565	212	398	SRVRGCFPPNLPKSSCI*ECGQGAHAHA CNPSTLGGRGQIA*AQEFKTSQGNVAK PHLYKI
13422	27323	A	13566	26	395	YSPVHTDKCSGVRKLGLFFFFFKEKPH FFSPAWKARAKIGLNGTFLSQGKNFRP KPPKKRGKRGAPQPGKILNFKKKRGFS MGAKVNPNGPKGNPPP*PPKGAGKGG TPRPGPFFFFF
13423	27324	A	13567	400	195	ATRVSLAPTCKINWGWPTVPIPPPQE GEAGEFL*PQKWRVRLNKIVPLSPRPD

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						KTRLCFKKKKKN
13424	27325	A	13568	316	154	SQPFPLRWEDRLSRGVNQPKQ*LMPV IPAFSGAEVGGSLPRSSKPA*ATNNLK SKVIIGGQICDKASKVSI VESSWWGWC
13425	27326	A	13569	297	475	FDYFFIY*ETKSHSAAQAGVQ*CKHSSL QP*PPGLKQSLLPWPPKSAGLTGVS YGT WPI
13426	27327	A	13570	116	332	NRVLLLPKGEYRGTTISAHCSLKLGLSKR PPTSAA*GDETTGVCHHTPV*FLKTFF IEIRPGYVPRVGHWR
13427	27328	A	13571	233	405	TVPELRASCRLKKKKKKKKEKNLKKIK GFPFGPGRV*GPEAKNPGGGGPGIPKGP G
13428	27329	A	13572	408	3	TFCDYFKTPPPGKFFFFINGPPSFFLNRG PSFFFFPGFPPFLKNFFFFPLVVKGG GYKRGVFPKKKGPPQPLFFFFFFFLI* KKTRPGTVAHPCNPSTLGGQGRWIT*GQ EFLSSLAKMAGRVVRPGNCESV
13429	27330	A	13573	273	406	IKBFKAERGGHS*NTSTFGGQGRWIA*S QEFETSLANMVKPHLY
13430	27331	A	13574	385	38	KKNSPPPPGKNFFFF*GPPSPFFFFF FFFFFFFFLGGKKTFFPPPSRFFFFFLKP FPPKNQGPKNFFPPKKKIGD*ARPPPLT GGAKGAPLEFKKKKKKKLKVPRGAVAHT CNS
13431	27332	A	13575	230	53	HWKVLKENKQIFTKISFKMNAIKDSVGQ AQWLMPVIPAL*EPDMGGPVEPKSLRPA WAT
13432	27333	A	13576	406	33	VNSIVWVSSPFRVSTFISFFELKSCSVT QAGV*WHDLSLLQLQTPGLKRS PAPS RG LSFYLLSSIFYPHSSQTELFVGT LNAASF TNSRLLYLSLLLCGYHPLVPSLPLSTI WYFSLRVSHHP
13433	27334	A	13577	426	294	GGFSPFPVFKPPPQFFFFGLPKKISPP PPGEKKIFF*KAPPP
13434	27335	A	13578	268	3	LQAKGPAMGEAGARCSSEVWGWRPKGFD L*VSR*PSFDSHVRIGRVQLMPVVPVL WETEADISFEPCCSRPAWASWRKTYIQK PQRI
13435	27336	A	13579	395	49	EKKKFFVCFPFGFPGNPPNPSPQFF*KGL ISPSGSLRTRRGFFP*RVFFFLKKQFP LSPRVECNGIIPDP*PPFGEVTSTPQVA GAIGPPPPRVNFYFFVKGFNLVNGPMF FFF
13436	27337	A	13580	68	466	GASPAQGSTLHLVLPRYFFKIPTVRTE SFGSLVTSPPPLHFLPLNKERGGPGI P LPCPQLQLVLGGTSLPPVPSLPDTSQDK WPLHGVPPGHVCS*PLAGDGAWPPSPHW IPLNPGTSKSLQAPPPWNSA
13437	27338	A	13581	67	249	ATAPGLLCYKIFSCQLQWCVPTQLAW ETEAGGSLEARSSRL**TMITPVNRHCI LAWAT
13438	27339	A	13582	359	3	KQDSQWVAAPASVAVSTCWRGLPLPWS GGQNRGKGSPLQVHRGA*GTENKNQGG TPRPGGGPGPSAPRGSSSLGAHRKLPVHH TTLSSRSALPPTPRHPAPSSPPCTEEF HRTRPI
13439	27340	A	13583	174	1	FFFFFFETESHVAQARVLEYS GAIPAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CNLDNLSSELPASAS*AS*VAAXTGT*KR
13440	27341	A	13584	192	206	LEFFLEVGSVCYVAQAGFEFFPGSGHLPISA S*VVGSTGVPHHTQLV*SFSSLYNLERN C
13441	27342	A	13585	244	28	KKPENQEINYIFYHLEFNVEHQIRISLGP GAVAYNCNPSTLRD*GGRIT*AQEFKTN LGNMARPRTRGSTRTF
13442	27343	A	13586	312	701	RGPEET*PRTRKSSPRPTRSCESVSKLA RPPRRCSAAPAQVPRLSLRSPKDPDP SSAEKCAPLPLLEPCSETGALPRNSFLC QNASSPLLSLGLPPSPPTVQALQPRALHQ HLGSTNKEDAHVAPAKK
13443	27344	A	13587	410	292	GYMIKQQTVYHECRM*ANSHLHLPPEGL LRAVTLWRRAP
13444	27345	A	13588	428	36	TPPPFFFFWAQKKKKIFPPPGGKIFFFL KGPPPLFFFFFFFFFFFFLKKFGLK GPPFFVQD*QGLENPKEGSSLGWEKLGR ALLPQQRSEFVPGGLPTRLFWGLVFWFFG FFFLPFGLCFFFALIFNC
13445	27346	A	13589	3	364	TAPDDQGRPYQAGEPAHVRASTHGLG A*RRVAGHLPPRVGAPHHPGASSREGAP PLHPPPNL*HRRPNGSCRFLPGPAAPPQ GAEGGRGRDRRGTHSVAQTGGPGGFGSG VTPSWRSS
13446	27347	A	13590	778	910	DRIRRSAGAHTCNPSTLGGQGERTA*G QEFKTSLGDMVRFCLY
13447	27348	A	13591	230	3	KLVNILVEKSLVAMKSTVSEGMVIRSP ASLGMVAHTHSPSTLGGQGRQIA*AQEF ETILGNMAEPCLYKKHSVY
13448	27349	A	13592	223	340	LTPPIPEPWESEVVGSL*LTPGAHTHA YNPRTLGRSGRIT*GHEFQTTLSHTMK TRLYHELL
13449	27350	A	13593	35	220	DRASLSPRLCSCGMIVAHCSINLSGSSD PLTPAS*GDGTTDTCHHARLI FTGADFC IDASS
13450	27351	A	13594	87	369	NVQKTECEISGKMQIWQKGSVKTKCSNG LFNFPIFSKKIASCKVKLTRE*KYKSQ ARWCTPVI PATEAEVRGQLEPRSLRP AW ATYQPHFKS
13451	27352	A	13595	261	489	SWVNERNMVG**KHETSQAQWLMPIIPA LCEAEVGGSLARSWETS LCNIVRLHLS KKKRGKGRKRGGNQIAPSRE
13452	27353	A	13596	238	2	NDCLWWLFRIPANVSTFGLLHMSLKVNT PGNNRFKSELGTRCLIHTCNPSILGGQG GWIT*GQEFVTSMQGS AVKNQ
13453	27354	A	13597	36	687	RDVHRSTYQAGSKQDWGPGEABRLSSSR RGAYSCPVPITFAEGKTRMGRDKMRLIL GLSWGPSLTLPLITNAPRRPGM*EPAL PGNSTS*SGAVRFPGGGRK*EDSAESWS CFCSHPSPPSGPNPPSPSAVCMPLPGLS GLQR*PKQLSPPPALSLPVSSLLVRLSP WPPTSSHLLPQALPQSLHPQGSRAVND SFSM*GMVLGSRNRRCMEA
13454	27355	A	13598	367	468	KKQRRGREPWLTPTALWAKAGGSP* VQSSRP
13455	27356	A	13599	183	380	LTSMLAVDNSSVEKTCQAMRISRPGAV AHTCNPSILGGQGGLIA*VQEYETNLGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MAKTHLYKN
13456	27357	A	13600	161	657	LIQGCWCSLFFSTRVFLAAIGMKSQWCR PVAMDLGVYQLRHFSISFLSLLGTENA SVRLDNSSSGASVVAIDNKIEQAMDVLK SHLMYAV*EEVEVLKEQIKELIEKNSQL EQENNLLKTLASPEQLAQFQAQLQTGSP PATTQPQGTTPPPAQPASQSGSPTA
13457	27358	A	13602	121	423	MIKVNSTGLYLYSQVIYIYIMKYVTAIY LKDFFFDGVLTRHPRWNTVTTQCSLEI LGSTDPPASAS*AAGTTNTSHHGQLYSY FKKRPTYAEMEYKIKK
13458	27359	A	13603	1889	1717	VPRIRPLSWTPPSSI*RPKPSSSTFSHP GKPSMGPPGLNRCVPQRALLPGWYQHCG R
13459	27360	A	13604	81	267	ETCCTIKNNTLK*I*SQMLWCAPIVPATW QAEVGGSLDPRSSSL*CAMITSVNNHCT PAWAR
13460	27361	A	13605	267	418	THASGMVTHTCNPGTLRVSAGRIT*GQE FKTSLGNIARPHLYKIIINKYI
13461	27362	A	13606	428	24	CPESNPRKREPTLKSEPIITLPITGLIL DDGNSPTAAAGSVFAETLQPPQCSSLCC* VKSSPWPTASLPQPFSGAPQTLPVRYAL IPGPSLVSTSLGPRAPGLPGSPSPSPSP QVTLDSEYRPSPTPCIAPALED
13462	27363	A	13607	267	442	RPPPTLKVPLGVVEVHACNPRTLGGQGG SIS*AQKLENSLSNILRPHLYQKQKQKQ KK
13463	27364	A	13608	3	280	YRLSVICEDPMREREQTCFPPPPSFPN RYCSTRDGGMEGSQGDFRKGFP*APCR SGGGWRGCCSPAGAPGSPLCGSSQGGPV SPWGQKRS
13464	27365	A	13609	291	248	EKRAHGSQPMKGRERNMCKSSSEFRVVA WSLAGVKGDGGR*GSGAGGSPKLG*AV* LDPEGHAGQAVFCGEAGARTQIGGKG*R RDQAPLPLSPNLCSGSCLPTKHS LAMP LRVKSYSQAQLGRTTCTRPSPPTITFDS S
13465	27366	A	13610	267	3	HTDLLYNTPTHPISPRCDPKHTAIPDKQ SLLFFFFEMESCSVARAGVRWHDLRSLR PLPPRF*KFFCCSIPSLYCGRSRGSSQT YTS

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13470	27371	A	13615	197	428	KTMVGLKTSASFHQDFIQIPLNHNLSVP *TMLGSQPRFLFPPGTVSHICNPSTLGG RGGWIT*GQEFETSLATMVKP
13471	27372	A	13616	445	550	TSITRGRARWLTPVILVLWEAEAGGSP* GRSSRLP
13472	27373	A	13617	3	435	TMVLSPADKTNVKAARWVGAGHAGEYGA EALERMFLSFPTTKTYFPHFDLSHGSQAQ VKGHGKKEADALTNAVAHVDDMPNALS VLSDLHAHKLKRVDPVNFKLLSHCLLVTL DRLPAEFTPAVHASLDKFLASVSTVLTS KYR
13473	27374	A	13618	719	918	CEGRREKWKIGRERKGRGRKGEQMGRE GKGREDGGRRKPCTSRPRSSSRDRSNI I ISEHASAVEA
13474	27375	A	13619	847	938	WLMPAVPALLEAEVGISLEAQSCRPPWA TQ
13475	27376	A	13620	349	409	NLWSWPGAVAHVCNPSTLGG
13476	27377	B	13621	25	189	MVLSPADETNVKAAWGKVGAGHAGEYGA EALERMFLCFPTTMTYFPDFDLIHGSAQ*
13477	27378	A	13622	142	356	RIVENEKINAESKSKQKVDLQSLPTRY LDQTVVPIILLQGLAVLAKERPPNPPIEFL ASYLLKKNKAQFEDRN
13478	27379	A	13623	18	1353	AGAAQCEVVSAGEAGARTMSEADGLRQR RPLRPQVVTTDDGQAPEAKDGSSFSGRV FRVTFMLAVSLTVPLLGAMMLLESPI DPOPLRQISGIALFCSFKEPPLLLGLV LHPNTKLRQAERLFENQLVGPESIAHIG DVMFTGTADGRVVKLENGEIETIARFG SGPCKTRDDEPVCGRPLGIRAGPNTL FVADAYKGLFEVNPWKREVKLLLSSET PIEGKNMSFVNDLTVTQDGRKIYFTD SSSKWQRDYLLLVMEGTDDGRLL EYDVTREVKVLLDQLRFPNGVQL SPAEDFVLVAETTMARIRRVYVSG LMKGGADLFVENMPGFPDNI RPSSSGGYWVGMTIRPNPGFSMLD FLSERPWIKRMIFKLFSQETVMKFV PRYSLVLELSDSGAFRRSLHDPDGL VATYISEVHEHDGHLVLSFRSPFL CRLSLQAV
13479	27380	A	13624	18	1353	AGAAQCEVVSAGEAGARTMSEADGLRQR RPLRPQVVTTDDGQAPEAKDGSSFSGRV FRVTFMLAVSLTVPLLGAMMLLESPI DPOPLRQISGIALFCSFKEPPLLLGLV LHPNTKLRQAERLFENQLVGPESIAHIG DVMFTGTADGRVVKLENGEIETIARFG SGPCKTRDDEPVCGRPLGIRAGPNTL FVADAYKGLFEVNPWKREVKLLLSSET PIEGKNMSFVNDLTVTQDGRKIYFTD SSSKWQRDYLLLVMEGTDDGRLL EYDVTREVKVLLDQLRFPNGVQL SPAEDFVLVAETTMARIRRVYVSG LMKGGADLFVENMPGFPDNI RPSSSGGYWVGMTIRPNPGFSMLD FLSERPWIKRMIFKLFSQETVMKFV PRYSLVLELSDSGAFRRSLHDPDGL VATYISEVHEHDGHLVLSFRSPFL CRLSLQAV
13480	27381	A	13625	1	384	QSFRGTGRKRERERKRMSLSDWHLAAKL ADQPLTPKSIILRLPETELGEYSLGYSI SFLKQLIAGKLQESVPDPFLIDLIIYCGR KLLDDQTLDFYGIQPGSTVHVLRKSWPE

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13481	27382	A	13626	980	1089	PDQKPEPVDKEAMRD KRIRIQLTGLYPVPPPPPPQSPPIFP RPTSPTRT
13482	27383	A	13627	116	587	VCCELRADSWPVPSQPEQASGPQKQAFI WPEAPRSARLPITYTDYDWSRLQQTES QMLGSMARKKPRNTSRPLALNPLKSKD VLAVLAERNEAIVPVGAWEVSPSGSSE IPAYTSAYLIBEELKEQLRKKQEALKHF QKQVKYRVNQITLTKQ
13483	27384	A	13628	150	484	VAFPPQASRGVRKTEVGEQQGTACGGC GHQCPPTWHIQRACVPTCGAGWHL QGRASCRRPPSQSPQVYQTQVGRQDPHF GVGRDSRGELAWSSFIHPIYLLSVCNPL
13484	27385	A	13629	330	397	ARCEWLTVPVIALWEAEAGGSH
13485	27386	A	13630	10	137	SFTGAVILIIAHGLTSSLLFCLANSNYE RTHNLFFLNDFFFS
13486	27387	A	13631	380	98	FQWLVSFTATLWFEERHRKNKIEREERR AKGERGDRKEERREEGGERGRRGGERS DKREPKKKSKEESNHPKVVKFSFICSFC FLTPTFFPVFF
13487	27388	A	13632	56	827	PLFEAFTACGFVHDCGLLIHPEETCGLQ PISSDYIEAILQSELKRCPSGDMKGQWI VPCLSCSDNRTCDWREITWQPHNCQYGV LTKPQLQQCLGGRKILFIGDSTNRGIMY YLIERLNETLQEWQKVHGTKFYHNVNGG KTLISYSYYPQFWISPSLRPTFENALEH LLQRSRPLENTGQTVLVVGGVQWLSNH LQIIHKVLKSPFTTLNQPVTKSCLQAIY FPRLSPTLHSNCLDLVVSFTKSFNIYFV VQFLN
13488	27389	A	13634	3	2718	SGPCRTTVAPLLRAAPVEHCVAALRPTD STMLKKFDKKDEESGGSNPFQHLEKSA VLQEARVFNETPINPRKCAHILTKILYL INQGEHLGTTEATEAFFAMTKLFQSNPD TLRRMCYLTKEMSCIAEDVIVTSSLT KDMTGKEDNYRGPAVRALCQITDSTMLQ AIERYMKQAIVDKVPSSVSSALVSSLHL LKCSFDVVKRWVNEAQEAASSDNIMVQY HALGLLYHVRKNDRDLAVNKMISKVTRHG LKSPFAYCMMIRVASKQLEEDGSRDSP LFDFIESCLRKNHEMVVYEAASAVNLP GCSAKELAPAVSVLQLFCSSPKAALRYA AVRTLNVKVMKHPASVATCNLDLENLVT DSNRSIATLAITTLTKGSESSIDRLMK QISSFMSEISDEFKVVVVQAISALCQKY PRKHAVLMNLFMTLREEGGFYKRAIV DCIISIIEENSESKETGLSHLCEFIEDC EFTVLATRILHLLGQEGPKTTNPSKYIR FIYNRVVLEHEEVVRAGVSALAKFGAQN EEMLP SILVLLKRCVMDDNEVRDRATF YLVNLEQKQKALNAGYILNGLTVSIPGL ERALQQYTLPESEKPFDLKSVPLATAPM AEQRTSTPITAVKQPEKVAATRQEIFQ EQLAAVPEFRGLGPLFKSSPEPVALTES ETEYVIRCTKHTFTNHMVQFDCNTLN DQTLNVTVMQEPTEAYEVL CYVPARSL PYNQPGTCYTLVALPKEDFTAVACTFSC MMKFTVKDCDPTTGETDDEGEDEYVLE



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						DLEVTVADHIQKVMKLNFEAAWDEVGDE FEKEETFTLSTIKTLEAVGNIVKFLGM HPCERSDKVPDNKNTHTLLLAGVFRGGH DILVRSRLLLDVTVMQVTARSLEELPV DIIILASVG
13489	27390	A	13635	118	629	LWALQLHPEPELPSRRGTGAAGVWTGVA MIRFILIQNRAGKTRLAKWYMQFDDDEK QKLIIEEVHAVVTVRDAKHTNFVEFRNFK IIYRRYAGLYFCICVDVNDNNLAYLEAI HNFVEVLNEYFHNVCELDLDVFNFKVYVT VVDENFLAGEIRETSQTKVLKQLLMLQS LE
13490	27391	A	13636	57	221	LHHCTPPWAEVEETLKRQLSQKGVQGI VVNTEGGWEPLGHCGDRSRPPAQGCP
13491	27392	A	13639	344	544	LSGGHAGALSSSLWVHLYCLLSQQLLGN VLVTVLAIHFGKEFTPEVQASWQKMTG VCSALCFRYH
13492	27393	A	13640	319	623	DMEEASEGGGNDVRNQLQSEVEGVKNIM TONVERILARGENLEHLRNKTEDEATS EHFKTTSQKVARKFWWKNVKNMIVLICVI VFIIILFIVLFATGAFS
13493	27394	A	13641	2099	769	TRLAGRVSVASRPCRGPVAGGLLVERSK ARRPLLESERVAMAAPPELLQQEEDRSK LRSVSVDLNVDPSSLQIDIPDALSERDKV KFTVHTKTTLPFTQSPFSVTRQHEDFV WLHDTLIETTDYAGLIIPPAPTKPDFDG PREKMQLGEGEGSMTKEEFAMKQELE AEYLAVFKKTVSSHEVFLQRLSSHPVLS KDRNFHVFLFYDQDLSVRRKNTKEMFGG FFKSVVKSADDEVLTGVKEVDDFFEQEK NFLINYYNRIKDSCKADKMTSRSHKNA DDYIHTAACLHSLALEPTVIKKYLLKV AELFEKLRKVEGRVSSDEDLKLTLLRY YMLNIEAAKDLLYRRTKALIDYENSNA LDKARLKS KDVKLAEAHQQECCQKFEQL SESAKEELINFKRKRVAAFRKNLIEMSE LEIKHARNNVSLQSCIDLFKNN
13494	27395	A	13642	210	772	SVKMVRYSLDPENPTKSCSRGSLNRVH FKNTRETAQAIGMHIRKATKYLKDVTL QKQCVPFRRYNGGVGRCAQAKQGWGTQ RWPKKSAEFLHMLKNAESNAELKGLDV DSLVIHIVQVNKAPKMRRRTYRAHGRIN PYMSSPCHIEMILTEKEQIVPKPEEEVA QKKKISQKKLKKQKLMARE
13495	27396	A	13643	168	2172	SPLCEVSVPSFCFRVFCCKKHKHKSDKH LYEEYVEKPLKLVKVGNEVTELSTGS SGHDSLSLFEDKNDHDKHKDRKKRKKKG EKQIPGEEKGRKRRRVKEDKKKRDRLRV ENAEKDLQCHAPVRLDLPPEKPLTSSL AKQEEVEQTPLQEALNQLMRQLQRKDPS AFFSFVPTDFIAPGYSMI IKHPMDFSTM KEKIKNDYQSIEELKDNFKLMCTNAMI YNKPETIYYKAACKLLHSGMKILSQERI QSLKQSIDFMADLQKTRKQKDGTDTSQS GEDGCGWQREREDSGDAEAHAFKSPSKE NKKKDKDMLDEKFKSNLLEREQQLDRI VKESGGKLTTRRLVNSQCEFERKPDGTT TLGLLHPVDPPIVGEPPGYCPVRLGMTTGR

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						LQSGVNTLQGFKEDKRNKVTPLVLYLNVG PYSSYAPHYDSTFANISKDDSDLIYSTY GEDSDLPSDFSIEFLATCQDYPYVMAD SLLDVLTKGHSRTLQEMEMSLPEDEGH TRTLDTAKEMEQTIEVEPPGRLDSSSTQD RLIALKAVTNFGVPVEVFDSEAEIFQK KLDETTRLRELQEAQNERLSTRPPNM ICLLGPSYREMHLEQVTNNLKELAQQV TPGDIVSTYGVKAMGISIPSPVMENN VDLTEDTEEPKKTIDVAECGPGGS
13496	27397	A	13644	1032	207	PADVTPKPATEAVQSEHSASPMSINEV ILSASGACKLIDSLHSYCFSSRQNKSQV CCLREQVEKNGELKSLRQRVSRSDSQV RKLQEKLDLRRVSVFPYSSLLSPSREP PKMNPVVEPLSWMGLTWLSDPPGAGTYP TLQPFQYLEEVHISHVGQPMNFSFNSF HPDTRKPMHRECGFIRLKPDTNKVAFVS AQNTGVVEVEGEVNGOELCIASHSIAR ISFAKEPHVEQITRKFRNLSEKLEQTV SMATTTQPMTQHLHVTYKKVTP
13497	27398	A	13646	148	380	RGSWREVPEASLPSRGAKGKWRGLCCC CCCCCCCCCYHCHQEQGDLKHQADL WRSGRTQNQAGIWEHQHQTLEG
13498	27399	A	13647	2099	769	TRLAGRVSVASRPCRGPVAGLLVERSK ARRPLLESRVAMAAPPELLQQQEEDRSK LRSVSVDLNVDPSLQIDIPDALSERDKV KFTVHTKTLPTFQSPFSVTRQHEDFV WLHDTLIETTDYAGLIIPPAPT KPDPDG PREKMQKLGEGEGSMTKEEFAKMQELE AEYLAVFKKTVSSHEVFLQRLSSHPVLS KDRNFHVFLFYDQDLSVRRKNTKEMFGG FFKS VVKSADDEVLTGVEKVDFFFEQEK NFLINYYNRKDSCKVADKMTSRSHKNVA DDYIHTAACLSLAL EEP TVIKKYLLKV AELFEKLRKVEGRVSSDEDLKLT ELLRY YMLNIEAAKDLLYRRTKALIDYENS NKA LDKARLKS KDVKLAEAHQQECCQKFBQL SESAKEELINFKRKRVAFRKNLIEMSE LEIKHARNNVSLQSCIDLFKNN
13499	27400	A	13648	1	1206	MSTSQSPCESICDYVTS HDKSNFTDMIK LNILRCEVILDYPAPGGGSLGAKHCCSC YTVSSGVTEGERNAGEKGVKLNADGARI RGTPGRGRRAEAEASSPAPA VAAACVV AAAAASRQLASGNRTRVSSGVPAFLG TMNPNCARCGKIVYPTKVNCLDKFWHK ACFHCETCKMTLNMKNYKGYEKKPYCNA HYPKQSFTMVADTPENLR LKQQSELQSQ VRYKEEFKNGKGFVSVADTP ELQRIK KTQDQISNIKYHEEFKSRMGPSGGEGM EPERRDSQDGSSYRRPLEQQQPHHIPTS APVYQQPQQQPV AQSYGGYKEPAAPVSI QRSAPGGGKRYRAVYDYSADEDEVSF QDGD TIVNVQQIDDGWMYGTVERTGDTG MLPANYVEAI
13500	27401	A	13649	3	394	GDGGGHLGSGRNGGSGMNAPP AFESFL FEGEKITINKDTKVPNACLF TMNKEDHT LGNI IKSQLLKDPQVLFAGYKVPHPLEH KIIIRVQTTPDYS PQEAF TNAITDLISE

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13501	27402	A	13650	1	471	LSLLEERFRVRAGPGGAD SRPTGLREAGSGPREAPRRSGCKSPGL GTVGMLRPKALTQVLSQANTGGVQSTLL LNNESLLAYSGYGD TDARVTAAIASNI WAAAYDRNGNQAFNEDNLKFLMDCMEGR VAITRVANLLLCMYAKETVGFGLKAKA QALVQYLEEPLTQVAAS
13502	27403	A	13651	1334	82	CYTGGTQSLWPGSSCASSVARPSSLFRS AWSCEWSVRCARACTMSVPAFIDISEED QAAELRAYLKSKEAIESENSEGGHLVD LAQII EACDVLKEDDKDVESVMNSVVS LLLILEPDKQEBALIESLCEKLVKFREGE RPSRLQLLSNLFHGMKDNTPVRYTVYC SLIKVAASCGAIQYIPTELDQVRKWISD WNLTTEKKHTLLRLLYEALVDCKSDAA SKVMVELLGSYTEDNASQARVDAHRCIV RALKDPNAFLFDHLLTLKPVKFLEGELI HDLITIFVSAKLASYVKFYQNNKDFIDS LGLLHEQNMAMRLLTFMGMAVENKEIS FDTMQQELQIGADDVEAFVIDAVRTKMV YCKIDQTRKVVVSHSTHRTFGKQWQQ LYDTLNAWKQNLNKKVNSLLSLSDT
13503	27404	A	13652	1	377	TTASGRSGVKGSTMSAEVPEAASAEQK EMEDKVTSPKAEAEAKLKARYPHLGQKP GGSDFLRKRLQKGQKYFDSGDYNMAKAK MKNKQLPTAAPDKTEVTGDHIPTPDLP QRKPSLVASKLAG
13504	27405	A	13653	424	596	SLKNIYGLSCRKKKKGAVKKIILVQAWW LMPVITVLWEAEVGGLEARGLRPTRAT W
13505	27406	A	13654	190	448	LRSYPAPHLGSPELRIRKGRGHSHCLAG AAGPQRTALCGLSAPLCPPSPTPPGAGA PRYCSGSDAPPCLLRGAGPPIPGMGDPE TS
13506	27407	A	13657	1612	563	SMPGWRLLTQVGAQVLGRLGDGLGAALG PGNRTHIWL FVRGLHGKSGTWDEHLSE ENVPFIKQLVSDDEKQALSKLCPLKDE PWP IHPWEPGSFRVGLIALKLGMMPLWT KDGQKHVVTLQVQDCHVLKYTSKENCN GKMATLSVGKTVSRFRKATSILEFYRE LGLPPKQTVKIFNITDNAIKPGTPLYA AHFRPGQYVDVTAKTIGKGFQGVMKRWG FKGQPATHGQTKTHRRPGAVATGDIRV WPGTKMPGKMGNIYRTEYGLKVRINTK HNIIYVNGSVPGHKNCVVKVDSKLPAY KDLGKNLPFTYFPDGDEELPEDLYDE NVCQPGAPSITFA
13507	27408	A	13658	128	2626	NSHRWVYVRARRRRRGKQREQPEDRGV PMKRAAMALHSPQYIFGDFSPDEFNQFF VTPRSSVELPPYSGTVLCGTQAVDKLPD GOEYQRIEFGVDEVIEPSDTLPRTSYS ISSTLNPQAPEFILGCTASKITPDGKITK EASYGSIDCQYPGSALALDGSSNVAEV LENDGVSGGLGQRERKKKKRPPGYYSY LKDGGDDSI STEALVNGHANSAPNSVS AEDAEFMGDMPPSVTPRTCNSPQNSTD VSDIVPDSFPFGALGSDTRTAGQPEGGP GADFGQSCFP AEAGRDTLSRTAGAQPCV

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						GTDTTENLGVANGQIILESSGEGTATNGV ELHTTESIDLDPKTPESASPPADGTGSA SGTLPVSQPKSWASLFHDSKPSSSPVA YVETKYSPPAISPLVSEKQVEVKEGLVP VSEDPVAIKIAELLENVTLIHKPVSLQP RGLINKGNWCYINATLQALVACPPMYHL MKFIPLYSKVQRPCTSTPMIDSFVRLMN EFTNMPVPPKPRQALGDKIVRDIRPGAA FEPTYIYRLLTVNKSSLSEKGRQEDAE YLGFILNGLHEEMLNLKLLSPSNEKLT ISNGPKNHSVNEEEQEEQGESEDEWEQ VGPRNKTSVTRQADFVQTPITGIFGGHI RSVVYQQSSKESATLPFFTLQLDIQSD KIRTVQDALES LVARES VQGYTTTKQE VEISRRVTLEKLPPVLVLHLKRFVYEKT GGCQKLIKNIYPPVDEISKELLSPGVK NKNFKCHRTRYRLFVAVYHHGNSATGGHY TTDVFQIGLNGWLRIDDTQTVKVINQYQV VKPTAERTAYLLYYRRVDLL
13508	27409	A	13659	42	382	TLWLKTIQIYLTISLGLGSDYGLAGFSA LGCHQAAVKMLTAFILIQGLDLGRSHFQ AHSGCWQDSFP CDSRIHGGLLHVQQES PWFQSAERVSCITKCNHRSDTHLCSIL L
13509	27410	A	13660	178	349	DMGPCYVAQTVLKLGLSSDPPTSASQEA GTTCHHAHLLSHPPFLMIYRNFSTIQCLE T
13510	27411	A	13661	268	2	RQQKVILSSSGSLMSEMGRITVLPKSPG MNPSSPLLASGGCWKSLACGHIIPSSSF ILMWPSPLCVSVSSSLPMRKPLLHLRS TLFQ
13511	27412	A	13662	112	483	AGVGALRMVQRLTYRRRLSYNTASNKTR LSRTPGNRIVYLYTKKVGKAPKSACGVC PGRLRGVRAVRPKVLMRLSKTKKHVSRA YGGSMCAKCVDRDIKRAFLIEEQKIVVK VLKAAQSQKAK
13512	27413	A	13663	2	873	SVEEFDRGCTGRGCGADARAGAAMVKIS FQPAVAGIKGDKADKASASAPAPASATE ILLTPAREEQPPQHRSKRGSSVGGVCYL SMGMVLLMGLVFASVYIYRYFFLAQLA RDNFFRCGVLYEDSLSSQVRTQMELEED VKIYLDENYERINVPVQFGGDPADII HDFQRGLTAYHDISLDKCYVIELNTTIV LPPRNFWE LL MNVKGTYLPQTYIIQEE MVVTEHVSDKEALGSFIYHLCNGKDTYR LRRRATRRRINKRGAKNCNAIRHFENTF VVETLICGVV
13513	27414	A	13664	118	3	AWSLIPVIPVVREAKAGGLLEPRSLRPT WATWQDPVST
13514	27415	A	13665	1	2876	IRQRINFSRKNKWDSRKLQAGVSELAT NQKLILVCGRYEGIDERVITQTEIDEEWS IGDYVLSGGELPAMTLIDSVSRFIPGV GHEASATEDSFAEGLDCPHYTRPEVLE GMEVPPVLLSGNHAETRRWRLKQSLGRT WLRPELLENLALTEQARLLAEFKTEH AQQQKHHDGMAADEAGRTFLRADFNMIE EGDRI MVCLSGGKDSYTMLEILRNLQQS APINFSLVAVNLDQKQPGFPEHVLPEYL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EKLGVEYKIVEENTYGI VKEKIPEGKTT CSLCSRLRRGILYRTATLGATKIALGH HRDDILQTLFLNMFYGGKMGMPKLMSS DDGKHIVIRPLAYCREKDIQRFADAKAF PIIPCNLGSGPNLQRQVIADMLRDWDK RYPGRIETMFSAMQNVVPSHLCDTNLFD FKGITHGSEVVNGDLAFDREEIPLQPA CWQPEEDENQLDELRLNVVEPDGPRHRH APDARRFCQYLRHQARYLLSVVPNLDVA VTEPLANGDGLNVLIKREVVGFRANTVE KTGENQYRVWPNEMPADLHKIRPHHPLN RNLDHFFPLDLTNSTFSGGYVHVLKGVL SDDLKLSFKQMGYVRRDSHRLMVTALP PACQLVQVALGCFALRLECEILGEVLAQ LGTSVLPAEELLQARRASGDVASCQRLA QDEEPPLPPRGSPAAAYRAPLDLYRDLQ EDEGEDASLYGEPSPGPDSPPAELAYR PPLWEQSAKLWGTGGRAWEPPEELPQA SSPPYGALEEGLEPEPSAFSFLSLRREL SRPGDLATPESSAAASPRRIRAEVGPAS AYRSVSEPPGYQGTQLPVPWRPAHPLLR HLSPAACCPLCSPARLPSPRLAACAAWR RPAALVATACTDGHSAQQPRGPALGQL GPRSRLGRQLPWCFSLLGRGLGLWLPC PWGSPGHSRGLES PGQPLLEVGLSVYGR LQQQQA
13515	27416	A	13667	76	289	SGTFASPCEMDPNCSCSPVGSACAGS CKCKECKCTSCCKSCCSCPVGCAKCAQ GCICKGTSKDCSCCA
13516	27417	A	13669	2	667	GRVDAEQSRLGATERAAAAAMNPEYDYL FKLLLLIGDSGVGKSCLLLRFADDTYES YISTIGVDFKIRTIELDGTIKLQIWDT AGQERFRTITSSYYRGAGHIIIVVDVTD QESYANVKQWLQEI DR YASENVNKL LVG NKSDLTTKKVVDNNTAKEFADSLGIPFL ETSAKNATNVEQAFMTMAAEIKKRMGPG AASGGERPNLKIDSTPVKPAAGGCC
13517	27418	A	13670	176	398	RILKTQLQENNQPTTTTKNRQKTRTDTL PKGIYRRHISLWKLGTWLTVPVIALCEA NAGGRLESRSSRPVWATY
13518	27419	A	13671	149	247	RKGLALSPRLDCSGAITVNCSLNLQGLS NIPI
13519	27420	A	13672	257	359	VASLHGWAQWLTPVIPTLWKTKVGEFFFE PRCSR
13520	27421	A	13673	142	1	HLKGSGLAKHQWLMPVIPALWEAEVGGG LEPRSSRPVWATLQDP ISS
13521	27422	A	13674	619	168	MFIESCTPKIYTSFVLRQSHSFAQAGV QWLDLGSLOPLSLGSSNSPASASCIQVL FVIYTSVKLGVGGRGLGNKKVMSSNKKFV CECRGWIILPFSVPSLRFQDGGWDHGVS SAEKALQAGRTAGHRVGVPPLGAPCGGA PCTTPPAWRS
13522	27423	A	13675	3	370	ARALLHPRLHQWQCLCHLQGTGGCPQQS PSSEGRADLLSPALEEGYPPASGCFIP HFLCGCSIFNCLPPIMRHAHKS PDALLE TLGP CRAWRLMPVIPTLWEAKVDRLLLES RSSRPSWPTW
13523	27424	A	13676	3	281	IGLRPELSVSLGRQRLTAIRLQPLLPAR

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						TPCGFLRARVAIALMADETDLPPLPRLE YSGMITAYCSLDFLGSSDPPTLGSGVAG TTENCCE
13524	27425	A	13677	272	389	YCRQIEKSKKKRCWLGTVAHACNPSTWG GRGGRITRSRD
13525	27426	A	13678	261	363	NSSWGHHARWLTSVIPALWEAEVGGSP EVRSLRPV
13526	27427	A	13679	149	44	SCVMSVSVLKKMYWLGAVAHACNPSTLG GQGGRTA
13527	27428	C	13680	118	267	MSHCTWLMCVVCVCVCVCVYAYMYTYSF LRWDLPLMLSRLECSGSQAQ**
13528	27429	A	13682	16	346	NHHLTQPHPHLDINDFFFFFFFFFFFFFFF FFFFFFFFFFFFLKKSPRAGKKKKKKKK KKKPPRFFFLGGAPPLFFFLINFFFFFF LCKIISLVYNRRGGPCLSKRFFLKERKS PL
13529	27430	A	13683	244	140	GRVDVFHHVAQAGLKLSSGDLPAWPPK ELRLQV
13530	27431	A	13684	191	777	NSDEHVYRCLYGHKLSFLSKYLKSGLA GVLLPLDAAVDMKEIEEQFANLHIVKCS LGTKEPTYLLGIDTSKTVOAGKENLVAV LCSNGSIRIYDKERLNLVREFSGYPGLL NGVRFANSCDSVYSACTDGTVKCDARV AREKPVQLFKGYPSNIFISFDINCNDHI ICAGTEKVDDDALFGGFGDARMEFLQN
13531	27432	A	13685	150	253	VGWGLWLVPVPAFWEAKMGESLDPRNL LPCWAT
13532	27433	A	13686	500	321	IEMGSHYVAQAGLELLSSSNPPTSVSQS AGIVGMSHHALAAISKSSDASITSHHPM TTP
13533	27434	A	13687	6	424	MSLLQCGGIRCFKMPEPAKSAPAPKKGS KKAUTKAQKKDGKKRKRKESYSVVY KVLKQVHPDTGISSKAMGIMNSFVNDIF ERIALGEASRLAHYNKRSTITSREIQTAV RLLPLGELAKHAVSEGTKAVTKYTSSK
13534	27435	A	13688	178	293	TGYSSQAQWLMTVLTATWEAEAGGSIQP RSLRPATQ
13535	27436	A	13689	663	144	KELSAVSAGIPHSCGSGCGGGSVAACV PAAPAAAGLCSGRAQKVPVPPSLAGWPP GVNAPPPVPCSSVRLHVCQSDRLWVRLA ARRGILALLRSALKAAATLAGCQSVRWSV RPSESLRPTSNAASLFRSSVPTVLSHSV PLAASLGKRRACGGREHASVAVYLSVCL SLPT
13536	27437	A	13690	125	3	FAHQGHAPGQAWLRLPVPVLRALG RPEPRSSRTARA
13537	27438	A	13691	136	24	GGPPPPPPPPPPPPPPPPPPPPPPPPPP FFPGKLQDQFYVVK
13538	27439	A	13692	144	1	MLKIVQSGECLTLKFNFCLLSLCTLFP TLIALTTLLPISPFIIL
13539	27440	A	13693	1476	380	NSWSTLASELTWAATSADPERKSQAAS AAMWATLPLLCAGAWLLGVPVCGAELC VNSLEKHFHFKSWMSKHKRTYSTEEYHHR LQTFASNWRKINAHNNGNHTFKMALNQF SDMSFAEIKHKYLWSEPQNC SATKSNYL RGTGPYPSPVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALSAIAIATGKMLSLAE QQLVDCAQDFNNHGCQGLPSQAFYIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YKNGIMGEDTYPYQKGDGYCKFQPGKAI GFVKDVANITTYDEEAMVEAVALYNPVS FAFEVTQDFMMYRTGIYSSTSCHKTPDK VNHAVLAVGYGEKNGIPYWIWKNSWGPQ WGMNGYFLIERGKNNMCGLAACASYPIPL V
13540	27441	A	13694	87	2	PGWAWWFTPVILALWETEAGGSPEFKSL
13541	27442	A	13696	130	2	CNIIIIIIQVCWAWWLMFPVIALWHAEP GGSPEVESSRPALV
13542	27443	A	13697	282	107	GLTKCPGTVCRLKLVVISYQLSTICLSM MEHSGTILAHCSLKLGLSSDPPTSRSRV AS
13543	27444	A	13698	198	3	CSITVNKVKVMTLFRSSMSLEIVCDIDL AVLRDLGLSLQDPPFRFTPLSCLSLPSS WDYRRPLV
13544	27445	A	13699	2	120	ARGDGVSLWLPRLKCNAGTSAHCNLRPT GSSDKNFKTRF
13545	27446	A	13700	60	341	PDMGLEDERKMLTESGDPEEEEEQEEL VDPLTTVREQCEQLQKCKVKARERLELCD ERVSSRSHTDDDCPEELFDLHAKDHCV ALKLFNNLQ
13546	27447	A	13701	6	540	KNSRTLGCQGGIRGSLCRPKPGVGGTQ TRAVRPVAVCSADSARPHLPLRRADMKDS LVLLGRVPAHPDSRCWFLAWNPAAGTLLA SCGGDRRIRIWGTEGDSWICKSVLSEGH QRTVRKVAWSPCGNYLASASFDATTCTIW KKLTLRIYNILRKLEACIKPLCCALKYK CLEEKQLHS
13547	27448	A	13702	239	346	AKRGWLMFPVIALWEAKVGKSLERPRIS PLWATWQN
13548	27449	A	13703	210	300	LMPVISALWEAKARGLLEPRTLPAWAT W
13549	27450	A	13704	141	440	PSAFEHFEEKINLYFLKFCISQGFPERQN NRDREIHRERYERDRERHRYERGLRE LAHVIVEAEKPHHRPFITWETLGCWWSG SVQVQKWPWEPGKLMV
13550	27451	A	13705	204	438	LLNVLLTQLFFLFLSLRQSCSVAQARGQ WYNHGSLLQPSHSGASNPPTSASQSVGTT GMSHDHGLFLHFSTLDIFSSL
13551	27452	A	13706	1707	1821	AKAGGSQHLEILANAVKPCLYWECKMAG PWWCAPVGG
13552	27453	A	13707	167	334	IRRANFKILTEIGWTQWLTPVIALWEA EGGGLLLEPGSPSLVFLFFILTTILMRKK
13553	27454	A	13708	224	344	KDTAMEEEIKDEKTKGPWLGAHACN PSTLGDQGRQIA
13554	27455	A	13709	1476	380	NSWSTLASELTWLAATSADPERKSQAAS AAMWATLPLLCAGAWLLGVPVCGAAELC VNSLEKPHFKSWMSKHKRTYSTEEYHHR LQTFASNWRKINAHNNNGHTFKMALNQF SDMSFAEIKHKYLWSEPQNCSTKSNYL RGTGPPYPPSVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALESAIAIATGKMLSLAE QQLVDCAQDFNNHGCQGLPSQAFEYIL YKNGIMGEDTYPYQKGDGYCKFQPGKAI GFVKDVANITTYDEEAMVEAVALYNPVS FAFEVTQDFMMYRTGIYSSTSCHKTPDK VNHAVLAVGYGEKNGIPYWIWKNSWGPQ WGMNGYFLIERGKNNMCGLAACASYPIPL

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13555	27456	A	13710	763	257	YEKILKLTADAKFESGDVKATVAVLSFI LSSAAKHSVDGESSLSSELQQLGLPKHA ASLCRCRYEEKQSPQLQKHLRVCSLRMNRL AGVGWRVDYTLSSSLLQIRGKSPWCHCG WKVATCPQGPQAPACLPFPSSKTKFPR SSLARTESRPKTLMKLPWAEKGVPRPV
13556	27457	A	13711	133	401	VLSKSGNPYWGSLSTNHEIKGQEGCAWQL TPVIPALWEAEAGGSLEPRSLRPANATS WLPREIKLDDLKNGCGPSKITQGGPMVA GSLKL
13557	27458	A	13712	212	74	RRINLAPPRVFLKGPPFFFFFFF FFAWGNPLFLFNSTFGRT
13558	27459	A	13713	324	141	DRVLPRLECSVITARYRLNLLGSRDPP TSASLIAGSTGTCHHAWLSFSYLFTYVF FIIL
13559	27460	A	13714	299	431	IRLIWLSAVDHACNSSTLGHHGVQMTKG QDFETNLANTANPHPY
13560	27461	A	13715	133	1	ILVVAWWDMPAIPVLWEAETEGLLERPS LRPAWATWKNTISTKN
13561	27462	A	13716	18	165	IPLHHTHTHTHTHTHTGYLLAISGTEFL SVLYMASERECRTYNMLNK
13562	27463	A	13717	119	1	KPNVSAQWLAPVIPALWEARVGVLEKFP RSLRPTWATQQ
13563	27464	A	13718	271	64	VLRGISTLNEILAKTRNPPLQILMKPRK RWGTVAHLRAPVGDQPDQHSETPSLLKI TKISWVWWRTPVI
13564	27465	A	13719	21	209	KDGPKGTTGGSETNESVEMTECCSVTQAG VQWHDLGSLQPPPPGFKRFSCLGLPSSW DYSRND
13565	27466	A	13720	391	151	RGFFLKGEKKKNFFPTIILGKKILGSPGK KGEKKKKRGKIFFFLKNPLGFFPKKKV LGEKKNPYSGVWGKKKRGP PHP
13566	27467	A	13721	109	2	RRLGVAHAACNPSTLGGVEGGSQGPNC GQVTQAS
13567	27468	A	13722	69	369	RDITLQADGAHSLFPTTPSLNAYIIIFSSP IGPHTHRPHYATPTYLPFYTNNLIIKKK KKKKKKKKKKKKKKKKKKKKGGGPF KKTPEGGAPIFGGGGK
13568	27469	A	13723	58	1208	FWNENSPASELAPNGGGSVTSVPRLEDY LTPQLYKLTGVEGPSRANSRDSFHDRK TYKTPSANMMVLKVEELVTGKKNGNEA GEFLPEDFRDGEYEAAVTLEKQEDLKITL LAHPVTLGEQQWKSEKQREAELEKKKLE QRSKLENLEDEIIIIQLKKRKKYRKT PVVKEPEPEIITEPVDPVPTFLKAALNK LPVVEKFLSKNPNPDVCDEYKRTALHRA CLEGHLAIVEKLMEAGAQIEFRDMLST ATHWASRGGNLDVLKLLNKGAKISARD KLLSTALHVAVRTGHYCAEHLIACEAD LNAKDREGDTPHLDVAVRLNRYKMIRLLI MYGADLNIKNACAGKTMPDLVLHWQNGTK AIFDSLRENSYKTSRIATF
13569	27470	A	13724	400	135	KWNGKELNGVDGIGWDWNEMYWKGLEFH ETEWNELERNGLEWNGMSWDGIKCNGIK WNGIECSGMLWNGMEICGMECPLMEWIR VEWN
13570	27471	A	13726	186	344	SASLGLWRCRCRRSLVHSVNLNVAQAGV



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						QWRDLSSLQPPPPSRLPWPPKVLR
13571	27472	A	13727	380	168	APPQKKVFSKFPQGGFFAPPNRKKLFF SPPRKIVPPPKFFLWAPLFFFFFFF FFFFFFFWYSRTDYK
13572	27473	A	13728	324	219	RIMFFIFFYFFFFFFFVFFLFFFFFKR PPFFY
13573	27474	A	13729	2	270	RLQEASLSPVPEILGGALPSAKRTSYLL LSTLCLLLSETASRGNSLTGLGHRSDHY NSVRSGGQSLYSACPIVTIHTGTCYGGK AKCK
13574	27475	A	13730	134	3	AVHRCKKWGRGWRLTPVIPTLWEAEV GGPLEPRSLRPALAT
13575	27476	A	13731	429	641	RKKAVCFMNDLICFLDNFTKNNVLSQAW WCVHLVPTIWEAEAGGSLEPRSLKLQCP VVAPVNNCTPAWAT
13576	27477	A	13732	188	32	IFFFFLFFYLFLLLLFFPRSRHCTLQP GQQSETRSQNKQKTKNKQTKNLP
13577	27478	A	13733	341	3	GTVTPEEPKMGDQTPRGLRPERTLGR LSTSES RVDPTPRVGSSGGRTAPWGP PRERGRVAGSSLHRACNFSTNTIISVG LWLTPIVPTLGRAEAGGSPEVRSSTHAS
13578	27479	A	13734	208	2	KLYKNFFFRFTKNPPLLKKGFYLYNFF FKKKKKIVKKKKKKKKKKKQKKKKKK GRPLAIKNYPRV
13579	27480	A	13735	16	212	EGVSLLLPRLECRGTISAHCNLRHRGR CTPASASQILRLKQENHLNLGGGYRD PIKLQRTAS
13580	27481	A	13736	22	214	PDRPALPTRPGGWITWGREVRDQPGQCG ETPSLLKIEKLAGCDGTCLEQNCLQNN SNNKVGIR
13581	27482	A	13737	386	51	WNSITQQALFEHLCSGHTSLPAVPCP HQACFPTLPLICRGIIAHCNLGLLGSS DSPISASPIDGNTGLHPHARLFSPLWY RWGLTMMPKRSLSPGLKPSSRLADAWV
13582	27483	A	13738	204	431	SQHFGISRADHLSSNVGDQPEQHGNKNS LYKYYKINQGWAWWLTVPVPLWEGQVG GSPEGKELKTPLRNLGKPHL
13583	27484	A	13739	69	159	IKKEALSWAWWLTVPVLPALWKANAGGSP E
13584	27485	A	13740	32	285	FFLSFFLFFFFFFGGGKKKTKKFFSQD FLGPPKILGGGGFFSFFGGPFLKKGK KSPQNLFFLKKNPPFFFPKPLWGF
13585	27486	A	13741	372	213	YRSCVLLQONPPLFYQSWWNFSLCVCVC VCVCVCVETGSLKKFLLTQKKKR
13586	27487	A	13742	29	237	TKRKGYKTNKGYWAWWLTVPVLPALFI AEGNLILQMOKQAQPEAGCVCVCVCA CMCVCVCVKVFF
13587	27488	A	13743	322	183	HTHTHTHTHTHTHTNPIHVFLLLLKY PKIQSHQFHISAFQDPLL
13588	27489	A	13744	305	373	VGWGWLTVPVLPALWEAKVGGG
13589	27490	A	13745	172	1	KNKIEQMKWEMRQEAVAHSCNPSTLGG QGEFETSLVNMMPCLYKKMQKISQVCS C
13590	27491	A	13746	285	1045	FQHPFGLSQSEMAAVKASTSKATRPWYS HPVYARYWQHYHQAMWMSHNNAYRKA VESCFLNPWYLPALLPQSSYDNEAAYP QSFYDHHVAWQDYPCSSSHFRRSQHP YSSRIQASTKEDQALSKEEMETESDAE

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						VECDLSNMETTEELRQYFAETERHREER RRQQQLDAERLDSYVNADHDLYCNTRRS VEAPTERPGERRQAEMKRLYGDSAQKIQ AMEAAVQLSFDKHKCDRKQPKYWPVPLK F
13591	27492	A	13747	2	305	GRVGSFSVRDVELSDPARERGEMPVAVG PYGQSQPSCFDRVKMGFVMGCAVGMAAG ALFGTFSCLRIGMRGRELMMGGIGKTMQ SGGTFGTFMAIGMGIRC
13592	27493	A	13748	2	305	GRVGSFSVRDVELSDPARERGEMPVAVG PYGQSQPSCFDRVKMGFVMGCAVGMAAG ALFGTFSCLRIGMRGRELMMGGIGKTMQ SGGTFGTFMAIGMGIRC
13593	27494	A	13750	238	423	AVSWDQLTWGTGVQEKKIQAQAWGLMPV IPTLWEVEVGGSPVKSRRPACPHGKTP FLLKMQ
13594	27495	A	13751	455	248	ISVGPGLFQLNFCFLPEYGTFLSEKFF IMETGSRFVIQAGVQWGSYSSPQPQFFG FESSLKPPHSGVK
13595	27496	A	13752	2	98	IPTPTIHTHTSHHTHTHTHTSFLYMP PDLK
13596	27497	A	13753	196	2	IWAPPKIFLKKPPLFFFFFFFFFFFFFFF FFFFFFFFIISFIPWPLTRKQKLSRWVF FKDSACSA
13597	27498	A	13754	917	379	KYKKCSLQKNLLVGCKKYSYLCYRRHKL HLVTHGERKKPAAVNSFFLFFSFFFLN LVRNTEITKKRVNLHETKADAESCNDQC TTSSETASELEQIRSGKHNSGKWAGEGA AGGRREGERMEWTEMRGARGRRGRER EMERARVRGGEEREKEIDLYKKVTSKIE ETKLGNNLLKL
13598	27499	A	13755	175	21	KKKNFFFPVRVILGPPKVFVKRAPLFFF FFFFFFFFFFFFFFFFLKKSWRPLAI
13599	27500	A	13757	234	341	ETGWVQWLMPVIPAVWEAEVGGLEPR LRAARAI
13600	27501	A	13758	1	365	PAPNRRGGHIQDRATNSTELGANQCFFF SERPPSLEKKTPEINKEPRPAPQPSNPG NLGTREGGDSWAGTTRCLRRDEGDTYR TEPPTALSWGQTRAFFFPALPAGKKRH RNLLKTQFF
13601	27502	A	13759	87	181	SHTHHTHTHTHTHTFYLVHVIHFDMEI LGL
13602	27503	A	13760	1	228	ARGERERERERERERERERERERERE RYREGGRLLLTMGEGETERATDLYHTPP PSIAWRLCEPRPRAGILCGRNIF
13603	27504	A	13761	383	197	RCDPPAWVSQSARITGVSYRAQPATSVL MGEEDFLEDVIAFVRLAPAVLLSKLSE VSVAMT
13604	27505	A	13762	276	57	YAVLGGGGGRKNLFVVFVFFLFFFFFFF FKKQGFGLMPLGEDRGPNMGFFYPFPMVG DKTKLPFKKKKKRPR
13605	27506	A	13763	377	209	PRPAYGPAFLFTEGFSWNPFQFQMESR SVAQAGVQWCYLGSLQPPPPWFPPTLLN
13606	27507	A	13764	160	202	MEKYNVHPHSGILHSHEKEQAALFTIAK RWRQPSYPSIDEWKNIMSIHTVEYITAM KRKNQLYSQ
13607	27508	A	13765	390	284	ESGGHFLSLSLSIYIYIHIYIYVCYIY THTSHTI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13608	27509	A	13766	350	41	YVILQENRNTQNRKLLPKSTELCMLLQ MLLFILNTTNYPLPLWQCYHRFCSFFLK TGSFYVTQAKVRWLTGMITVHCSLKL DSSHPPKWLVLQELATVAS
13609	27510	A	13767	330	156	KITQAWWCVHVVPDNRAEVTVGIRLGR MRLPLEGACTNCVPSWEKQDPVSHNEK K
13610	27511	A	13768	25	292	KCFFLSWRGGSRLQSQHFRPRRADHLR PGVPDQPGQHGFLLVKMSDKPDLSEVEK FDRSKLKKTNTEENLTLSKEIFFSLVG VNIQD
13611	27512	A	13769	585	680	KCLGSRTRWLTVPVIPTLWBAEAGGSLRP RSS
13612	27513	A	13770	488	359	PSPRERKFLPFFKXKKGWGP PPPPKKNR GRGPQQKEGPKPKP
13613	27514	A	13771	794	515	PDMGLEDEQKMLTESGDP EEEEEEEEL VDPLTTVREQCEQLEKCVKARERLELCD ERVSSRSHTBEDCTEELDFLHARDHCV AHKLFNNLK
13614	27515	A	13772	130	397	VVGLTPLCFMRLASLRHRSKPQARKTKK KKKKKKKKKKKKGGSLKKKIFGGAKKS GATKKKNFPKRGQNKKNPGFFKNEIFF GGGAI
13615	27516	A	13773	376	145	TRVGGGCSEQRLCHCTPSWATEPNVSN NNKIPLELFPSNQTFHFVRNWKRGNN WLSNYSISSTVTRHFPFLFQF
13616	27517	A	13774	1	247	GLQSLADLLSGLLQKVCPLSNGIMDL LLYYLFTFTGSCSVAQARVQWCEHGSL QPHTSASSDPPTSATTCHHARLIW
13617	27518	A	13775	376	145	TRVGGGCSEQRLCHCTPSWATEPNVSN NNKIPLELFPSNQTFHFVRNWKRGNN WLSNYSISSTVTRHFPFLFQF
13618	27519	A	13776	107	468	EKARSPERARDQEGGTERDRNSEREKIL PKLREELPWVSGGWRCPPHQQGWSHWED NPGWGIPTGPSVGWGEKKGPGEGRSHKY GTGRTKCELGVSIGNSAFTLLHFYFKH RKRRKQI
13619	27520	A	13777	125	2	NIFFPLFELYFFKCHWARWLTVPVIALW EAKEGGSPEVRSS
13620	27521	A	13778	166	74	GRICYSHSLSKHTHTHTHTHTSHISF IP
13621	27522	A	13779	1	341	ARGERERERERERERERERERERERE RERERERERERERERERERERERERE RERERLSFSLGGGALKKKRIFLCVTLE GKHLPLTHTGFFGENTHTLSMKTREGG FICAGGDERRSASVMRAYIYRECEPHTH V
13622	27523	A	13780	614	337	RRCSALCYRRHGNHKVKIRSKQGASVS PHEHLRILSLEVRNVGLGHSIFPHSLR MYVCMYVCMYVCISYLSIYLSIYLSIY LSISISSR
13623	27524	A	13781	390	158	VLIRLSWGRICFQAHSGCWQNSGSCSHK TEGLCLLLAGSCSWLLGGALKGWASKEE FYTMQHSQSDTLSPLPYSIH
13624	27525	A	13782	308	163	TKFYLLFFFFFFFFLFIFFFFFFFFLKKKF LFFIQGGGKIKTPGTLTFLG
13625	27526	A	13783	45	277	IASGRPFFFFFFFFLHLPFQAFVFGGGGGT PFEYQNFVAYIKGQGNPFLFGCGDLFN

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						APQLIKQLSQLGQKYPKPKPLL
13626	27527	A	13784	413	218	PNFPFFLFFSGKFFFTFQNLFPFGFFPPP GEGKAFPGQGCVPVGGGFAGPTFFFGPP AFPEILYFF
13627	27528	A	13785	1011	1368	IDWENDLTPMVLCHGPSIYNKYSFSQNI FPISANFFFLAHINLTLLQLVSELCHKI ILRHFIYIKPIKDILNLYLILPGVWLPDL CKSTAICRYLCVCIYIHLIYIHTHTHIH YTHIRL
13628	27529	A	13786	161	425	RWGSCYCPGYPHLKI FKL LLL LVLVLEM GVLPLLPRLECSGMITVHCNLEFLGTSY PPISVSQTKKKRPFTLPPLPNLQIGLP LRGE
13629	27530	A	13787	70	311	DLISITALVISPNKFYIYLSIYLSIYLS IYLSIIYLI FISTNLLWVLSLWETLNKT RLNLFLTIQNNIWNPKLLVSALI
13630	27531	A	13788	25	219	RNMAAATLTSKLYSLFRRTSTFALTII VGVMFFERAFDQGAIDYHVNCKLWK HIKHKYENK
13631	27532	A	13789	279	138	RRSLALS PRWDCGLQWRNLGSLQALLPG FTFFSCLSLPSSWDYRPF
13632	27533	A	13790	138	28	GGVVRWLTVPVIPALWEARVGGLLEPGSS KKERGGKEV
13633	27534	A	13791	133	7	YSCQRCLTHGQAQWLTTVISAPWEAKAG RLLEPRSVRS AWAT
13634	27535	A	13792	86	290	EHVHRTLIEASVSGWGWWLTPVISA AWE AEVGGSLGQEF EISLGKCS ET PSLTTT TTESLG SFAATS
13635	27536	A	13793	150	37	KTIYPSQARWLMVPVIPALCEAEVGRLL E PSSSRLAWAV
13636	27537	A	13794	216	77	PTQHPTEGYMIKQQT VYHECRMWANS HL CLLPEGLLR AVTPWCHAP
13637	27538	A	13795	251	347	VARAWGLAPVIPALWEAEVGGSP EGRSL KPAL
13638	27539	A	13797	177	274	VQWHMSVVP AIQEA EVGGSP EPRSLRPA WATY
13639	27540	A	13798	307	406	KFKKGWAWWLMVPVIPALWEAKAGGSP ES RSLRP
13640	27541	A	13799	194	3	FFFFFFFFFEMGSHYIVQARVQWLF TDA NIVHCSLQLLASSDPPVSTSQVGLQACA DDAQNP E
13641	27542	A	13800	333	198	LPSVFFFFFFQTESCSVTQAGVEWCDLGS LHSSLGNRRLCLKIK
13642	27543	A	13801	1	335	ETERGRERETERGRERETERGRERETER GRERERERERERERERDR EGRERQRGE GKKNRDREENRRRRETERVGDVVCVCPHP NLILNCSPYISHVLREGLGKTYLNYGGS FPTLCSG
13643	27544	A	13803	14	454	RVFFDRSRYSRTLGSTHASALLGILVY RSHLISSLLC LEGIILSLFIATLTILN THSLLANIVPIAILVFACEAAVGLALL VSKKKKKGAPVLKNPWGAQSLRGQARKY FFPYREPKNLPGNLGKEPFLGGGDILG QPPYKN
13644	27545	A	13804	1474	1661	TDFHNSHLKCKCKNCIFSTLNYYIRREH FSIVFIFCYICVVKVHYIRRELFRCLYF LLYMCC
13645	27546	A	13805	360	3	LWGKRGGPFSPPPFFFLLELFFFLKKMG

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						GGGFFGGFPWGPPEKEIFFFVFFWAPQK KKKKKPPPFIFWGGGPPFFFFPPPKQK KKKNKKKKKKKQKKKKKKKKRAARWPA RSRSSA
13646	27547	A	13806	1	425	RLGGVALRSAADGAFVSGEFCGGKLLRW CLVTDFFPDSCTTCSYSRRSTPGCSPGG SRGLSEGEGLSSVSLQSRVLSAMKHVLN LYLLGVVLTLLSIFVRVMESLEGLLESP SPGTSWTTRSQLANTEPTKGLPDHPSRS M
13647	27548	A	13807	5	313	EKPYLQGITFTSKTTHLIYEFTPYTIIV KEYSTNYVLLIGNTQITKIYHIVFRKFS MTPIYKFQDLAQWLTPVIPTLWEAKPGG LLEPRSLQSSYSLLIILIL
13648	27549	A	13808	182	314	VITQLDKTERAQWLMFVILVLYEAEVGG LLEAMSSRPAAWTKTW
13649	27550	A	13809	219	1812	LEPPESGAMSGFNFGGTGAPTGGFTFGT AKTATTTTATGFSFSTSGTGGFNFGAPF QPATSTPSTGLFSLATQTPATQTTGTF GTATLASGGTGFFLIGIGASKNLNSNTAA TPAMANPSGFGGLGSSNLTAISSTVTSS QGTAPTGFVFGPSTTSVAPATTSGGFSF TGGSTAQPSGFNIGSAGNSAQPTAPATL PLTPATPAATTAGATQPAAPTPTATITS TGPSLFASIATAPTSSATTGLSLCTPVT TAGAPTAGTQGFSLKAPGAASGTSTTS TAATATATTTTSSSTTGFAINLKPLAPA GIPSNATAAVTAPPGPGAAAGAAASSAM TYAQLES LINKWSLELEDQERHFLQAT QVNAWDRTLIENGEKITSLHREVEKVKL DQKRLDQELDFILSQQKELEDLLSPLEE LVKEQSGTTIYLQHADEEREKTYKLAENI DAQLKRMAQDLKDIIHLNTSGAPADTS DPLQQICKILNAHMDSLQWIDQNSALLQ RKVEEVTKVCEGRRKEQERSFRITFD
13650	27551	A	13810	134	263	KNSLFKKKNNGRPWPLMPVLPALWEAEA GGLEPRGLRPTWVT
13651	27552	A	13811	210	51	TLSHRKPISEAYFARVRGFILEVSETR NPPIGWTRWLTVPVLPALWEAEAGG
13652	27553	A	13812	241	139	LHEAGLAPMIPALWEVKVGGLLEPRSPR PAWASW
13653	27554	A	13813	539	256	RTTQMSTAAGFTEAPNWKQPRCPWTEEQ TNKMWSLHAMECASAMKWEVLIQPAVR MARENSRRKPGMDHDIWSVWSAGEWLP LGRSTGKGS
13654	27555	A	13815	63	369	VRETPKTHYLEEISSPASPTAIPQSL FSFFISPPSSLATGSGHSGHPVHSLHHP PETEPSVSVCLWAGPKVPPGAAGKGS SNPLVIRSLAPPASL
13655	27556	A	13817	258	3	AESAPPFSTNSLFFTHTHTHTHTHTH THSLRTRWAPSQVCRPQTSQRGCECVG PTAFAPSPTLLKPHHPSSHVHLPSQPRR
13656	27557	A	13818	516	665	WFKSGSFWLGMVAHTCNPSTLGGQGGWI TSGRSRTSVTTTTTSQTCA
13657	27558	A	13819	295	361	WLTVPVLPALLEAVTGGSLPR
13658	27559	A	13820	166	368	GWATQHSAYVVSSSSGALCLGESCS VTQAGVQWCDLSSPQSPHPGFRFLCLS LPSSWDHRGDL

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13659	27560	A	13821	133	530	RKYCGQCLNMLNNVSLSSGDQSRVAY RSSHGDLRPRASALAMVSGDGLVSRPE AIHLGPRQAVRPSVRAESRRVDGGGRSP REFDGRGRSRQARFSPYPIPAVEPDLLR SVLQORLIALGGVIAARISV
13660	27561	A	13822	76	1958	RQELIWPLCSPPQGDRLQKSWIFFRPV MADKLTRIAIVNHDCKPKKCRQECKKS CPVVRMGKLCIEVTPQSKIAWISLCT GCGICIKKCPFGALSIVNLPNLEKETT HRYCANAFKLHRLPIPRPGEVLGLVGTN GIGKSTALKILAGKQKPNLGKYDDPPDW QELITYFRGSELQNYFTKILEDDLKAI KPQYVDQIPKAAKGTVGSIIDRKDETKT QAIVCQQLDLTHLKERNVEDLSGGELQR FACAVVCIQKADIFMFDEPSSYLDVKQR LKAATIRSLINPDRIIVVEHDLVSLD YLSDFICCLYGVPSAYGVVTMPFSVREG INIFLDGYVPTENLRFRDASLVFKVAET ANEEVKKMCMYKYPGMKKMGFEFLAI VAGEFTDSEIMVMLGENGTGKTTFIRML AGRLKPDEGGEVPVLNVSYKPKISPKS TGSVRQLLHEKIRDAYTHPQFVTDVMKP LQIENIIDQEVQTLSSGGLQORVALALCL GKPADVYLIDEPSAYLDSEQRLMAARVV KRFIHLAKKTAFFVEHDFIMATYIADR IVFDGVPSKNTVANSPQTLLAGMKNKFLS QLEITFRDPNNYRPRINKLNSIKDVEQ KKSGNYFFLDD
13661	27562	A	13823	3	292	KCWDYVHEPPRPAPMQTYQVDLRCCFVS TINLLVCGERASLPVESLVFSGLAEBVW MKAVLAPSRESGKLVLQQVPEYAEAIWG ARPA CRGLVFSA
13662	27563	A	13824	245	91	YKVNFGPPRGSGFFRPPPPFFFEVHFHFF IIFFFFFFFFSSFFLGCFFMYV
13663	27564	A	13825	276	100	PGQKKKTLSPKKKSIYLYIHTHIYIYT HTHIYKYIFVCVYICVSIYIHTHIVPR IFS
13664	27565	A	13826	202	375	IYNTYIHTHTHTHTHTNVLYIQSGDC IYAVLLGELSFYIIFVFLSSLISILPHL TY
13665	27566	A	13827	278	34	KPRGLSPAGVSAQRAWGPHSCPRLPDPR TELQVRQIPALVGSSAFQGRGRKGPVG GSGPSRPRAPPQPRPGCCQCTLLQI
13666	27567	A	13828	62	307	GGARAIFLNVPHLKRPMFFLELCLSTKC PVGTEFALDSLRLYNSNTFCWVQWLMP TIPALCKAEMGGLLEARSIPAWAT
13667	27568	A	13829	386	478	NRIGMVSHACNPSTLGGQRRIMRSGDQ DHS
13668	27569	A	13830	364	484	NENIWLGWAWLMPVIPALWEAKAGGSL EVRGSGPAANMV
13669	27570	A	13831	33	486	PARSAEFGTRERERERERERERERERE RERERERERERERERERERERERERG VICVCPCALLCVRES DPLSOKKYCVCFV VVRYTESLALSPFCLGRCLALLIFLEGM WRKIWAPSLSLCVGALFFSQHPPPFWC LCVLSLVRPLPLSLSGGVFVSQRALI
13670	27571	A	13832	6	718	YSAVEFAMAGVGAGPLRAMGRQALLLA LCATGAQGLYFHHIGETEKRCFIEEIPDE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TMVIGNYRTQMWDKQKEVFLPSTPGLGM HVEVKDPDGKMLQVVLSRQYQSEGRFTF TSHTPGDHQICLHSNSTRMALFAGGKLR VHLDIQVGEHANNYPETAAKDKLTELOL RARQLLDQVEQIQKEQDYQRYREERFRL TSESTNQRLVWWSIAQTIVILITGIWQM RHLKSFFFEAKKLV
13671	27572	A	13833	17	130	RLQEFGRTRERERERERERERERERE RDTHSFLHG
13672	27573	A	13834	283	460	LVVRLAICKNYSLKRETEPGSVAHVYNP STLGGQGGRTARGQEFKTSLDNIARPPS LQK
13673	27574	A	13835	3	435	WPRFCTALQEFGRTRERERERERERE RERERERERERERERERATSLSRARPSF LFPSACVSHTPYVGERENLSLHTLKH TREKHSLSYTNASARDTRARFSEGRAPP IYSVYLTHGVFFFFFFSLCLSVRHAEG L AHV
13674	27575	A	13837	351	57	RTLHVHISKFTGNLSDLYVQSEWQDLGT ADLSIMTSVLHCLPSLESIKNTDSWPSS VAHTCNPSTLGGGRGCRDQHGQHSKQPS LLKIQKIARRCGG
13675	27576	A	13838	336	150	TFCYKKYLWGAHCFIFRTTGLPIKNFYF GQAWCLLPVISARWEAETGGSLEPRSLR VAWAS
13676	27577	A	13839	310	454	HCSLGLPQVLLIILYKILLGWARNLT PVIPALWEVEAGGLLEARSSRP
13677	27578	A	13840	163	297	IIFFLLDLKQGAMTIVVSIYLSIYLSI YLSIYLYTHLTWNTLQL
13678	27579	A	13841	33	316	LDQHPTPRSPLLCHSLRKTSSSQGGKSE LVKQSLKKPKLPEGRFDAPEDSHLEKEP LEKFPDDVNPVTKEKGGPRGPEPTRYGD WERKGRCIDF
13679	27580	A	13842	4474	2586	DGGSGCVKMEFPGGNDNYLTITGPSHPF LSGAETFTPTSLGDEEFPIPIISLSDP SLAVSDVVGHFDDLADPSSSQDGSFSAQ YGVQTLDMFVGMTHGLMEQGGGLLSGGL TMDLDHSIGTQYSANPPVTIDVPMTDMT SGLMGHSQTLTIDQSELSSQLGLSLGGG TILPPAQSPEDRLSTTPSPTSSSLHEDGV EDFRRQLPSQKTVVVEAGKKQKAPKKRK KKDPNEPQKPVSAAYLFFRDTQAAIKGQ NPNATFGEVSKIVASMWDSLGEQKQIY KRKTEAAKKEYLKALAAKDNQECQATV ETVELDPAPPSQTPSPPPMATVDPASPA PASIEPPALSPSIVNSTLSSYVANQAS SGAGGQPNITKLIITKQMLPSSITMSQG GMVTVIPATVVTSRGLQLGQTSTATIQP SQQAQIVTRSVLQAAAAAAAAAQMQLPP PRLQPPPLQMQPPPTQQQVTLQQPPP LQAMQQPPQKVRINLQQPPPLQIKSV PLPTLKMQTLVPPTVESSEPERPMNNSP EAHTVEAPSPETICEMITDVVPEVESPS QMDVELVSGSPVALSPQPRCVRSGCENP PIVSKDWDNEYCSNECVVKHCRDVFLAW VASRNSNTVVFVK
13680	27581	A	13843	54	251	EFYRMNSPSPLWLCVCVCACLFMCLC ALTCMCVWYKSLLSNLTVLSSKPYDS

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						ISPAENPGK
13681	27582	A	13844	154	26	DPHVPPTERSEGSQARWLPPVIPTLWEA EACGSPEVKSSNST
13682	27583	A	13845	475	225	GHTELYGGALFQLLQAAIPEGGGTSCLF NPSSDGGSSAAGGVGGAGDLARSSRPV SPTSSRPVSPDPSPPSLYLTPWKETH
13683	27584	A	13846	479	319	RDCRRSLTHSVLSGAQAGVQWRDLGSLQ PPPPSRLPWPPKAPRWQPLPGHHPI
13684	27585	A	13847	182	499	LLCVKLCDSNENKALREQTRAQVQGGH SRAQVQVQGGHSAHTVVQIRSAASRRK AFSTCSSHLGMVLLFYGTGSSTYMRPTT RYSPLLEGRLAAVFYSILIPTLN
13685	27586	A	13848	388	494	RDSWERWLEPLIPVLWEAQAGRLLEPRS LRLAWAT
13686	27587	A	13849	198	63	HHATTWMNLEDIMFRKVSQTQKNKYMI PLIWKTKKVLSHREQK
13687	27588	A	13850	555	353	RCPPGAQAPLPAPSPAPVHIALSPLSC GVSWPRELTAHPPEPPPPFFFKIHPHPQ LSVGKRGQMTF
13688	27589	A	13851	169	66	LLAGSTGQARWLTPVIPELWKAIEVGGSL EIRSSR
13689	27590	A	13853	12	105	IASGLHDDFFKKKKIKKKKKKKKKKKGG AL
13690	27591	A	13854	256	363	ICLFIKDSDRGQTQWLTPVILTILWKAEA GGSLEPKS
13691	27592	A	13856	23	436	IDRLSDSHEERERERERERERERERERE RERERERERERERERERERERERERE RERESSLLCVRHTCFAPPTYIFLWETLR VCPTPCVWGALSVFSHTERARIFFTCG GSVARAPVCAHTRIFSSRARARALCARP PLSRERRAHTRVFFI
13692	27593	A	13857	91	428	PDPDTSPLTDRGETPLGATLPSCYCGG QSFEPKTKKTTNQKKKKKKKKFTPOKK NPKIFPPKPFCKPGPRGENQPKKTQNP KKKKKILGGGPAPNSPLGGGKKNSWAGF
13693	27594	A	13859	465	43	KRVTTENPOHICSAETAIPWSLSQNCN HILWGHGPNHPIYITTSIYIYIYIYIY GMVYIYTRICMCVCIYVHICHTHTHIY IYIHTHTHIYMERERTVSCSVAQAGVQ WCDLGLQPPNKRLLKRFSCSLSPSSWDY W
13694	27595	A	13860	290	52	WYKYLPGTRGFLIWLNLKICIGRIELLV GYFSFIYLSIYLSIYLSIYLSRSSIAQP GVKRCNHSSLQPRTPGLMHLNSNS
13695	27596	A	13861	108	22	IFFLFSAVKTRFSYAFPEFFPYRMNHVS I
13696	27597	A	13862	167	33	VFTVPGTYMCVSVDLQAWWLTPVIPA LWEAEAGGSLEEFLRT
13697	27598	A	13863	448	355	FFFFFFFFFFFFFFFFFFFFFAKN PLN
13698	27599	A	13864	321	445	SQSTQAWCLMPVIPALWETKSSESFEPR SLRPAWATGHNP I
13699	27600	A	13865	380	80	MILSPSPKFPFSFLFSALLLWHCLEL PFLSNVKGQMNDPVLSPSTSPDLSR IYLFCCFFVCLFVCFETGFPSVAQAGVQ WCDPLGLKWLPPQSP
13700	27601	A	13866	372	264	KMENPEDKNFFIFFMFFIVFLFFFFFL FCLTQFF



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13701	27602	A	13867	161	304	LFIAEMTSHYIAQAGLELLASSNPPTSA SERTGITDGGATEILPQLRL
13702	27603	A	13868	230	348	VSFQNLVFCVERVYRVPDFGVWERSK YNNGSTELHSK
13703	27604	A	13869	168	260	EVIAECYNGCFQTLSLCVCVCVCVCVCV CY
13704	27605	A	13870	140	16	LKYGQWRDLGSLQPPPPRFKQFSCLSLL SSRNCTTMRDHE
13705	27606	A	13871	143	30	KILKVVVSQAWWLIPVIPALWEAEVGG LEPRISRLA
13706	27607	A	13872	158	59	HLHGCIHLLKLRLDAVSHACNSSTLGGQ GGRIA
13707	27608	A	13873	232	115	APFFFKGAPIFFFFFFFFFFFFFIFFFLIR GKPGNDVGVG
13708	27609	A	13874	1619	1375	KTWRRHLEKLQDMSLLRHRVHVDSSQG LFPFFQROGLLPRLKCNIGDIIPYCNLKL LGWSNPSAFAFRVARTTSLCRHTWL
13709	27610	A	13875	219	84	NPLQSTSTICNRAWDRVTCWSQLLRRL RWEDHLSPGVPSCSAL
13710	27611	A	13876	166	496	KKKKKKKKGGGGLKKTGGAKINRGRK KKIFFQKGGQKKTGGILKKPFLGGGK KGNPPKKIKGLREKKKFKRGKAKPAQ NPWGKKISPPGFLLKFFPRGRGFFI
13711	27612	A	13877	132	348	PSKKKKRGGPFKRTPGGPKFNGGGKGN FPLMGGGIKPNLGLGNPYLGGGTNGN NPPTIKGFGKKKF
13712	27613	A	13878	287	134	QQGPPISPGPKENRMGPPSPGWGNGPI RSPPGAGPNPGAFQDGMFSPKKQ
13713	27614	A	13879	333	480	VHPLRSAEGPRPESNMLHLTKSKQWL TPVIPALWEAKAGGSQGEIE
13714	27615	A	13880	1	227	PKIHCKIQHIVVLVSFFPSFFLSFFQGE SCSAAQAGVQWHDLSLQAPPFGKWF FIELLGLGFHSRRMRGKDS
13715	27616	A	13881	276	378	GWPWWLTPVIPALLEAEVGGLEPRSLR LALAT
13716	27617	A	13882	126	389	GSVLGTGCCSVLGTVCGRSVLGTVLIA SATPDRLRLSSGSSLRTITNSDLVPWL TPVIPALWEAEAGVSLEPRIWRPARETW EDPH
13717	27618	A	13883	414	150	ARQAPKWGNPTGSPPPGFLNPPPKNFFL GPQKKKIFFPTPPPHFFFKGPPPPFF FFFFFFFFSPHAGSILLCHPGRIAVASW LTE
13718	27619	A	13884	197	363	DLGVVVNTFMLKFKCLNVSRGHVQWLI IPVIPILWKAZAGRSCLKPRSLRPAT
13719	27620	A	13885	101	236	NIHYANFPYFGLACPEYIVRALQKKYTQ THHTHTHTHTRTTHSL
13720	27621	A	13887	17	140	TVHLKMKVIGLHMVAHACNPSTLGGRG PIMRSGALGNFCL
13721	27622	A	13888	135	1	VLHAGLKLGSSTSPTSASKGAGTVGIH YHTQLAFQFLFCFLIR
13722	27623	A	13889	411	276	TLYFKHGMGFHHVQAGLELLASSDPP ALEFETSLHNKVRPRL
13723	27624	A	13890	216	54	EFKLCYTLFDHSYFPLEELVSGQVWRLR PAIPSFWEAKEGGSLEPRSSKHEIV
13724	27625	A	13891	3	149	SSDPRPSSSWLAWVGLWSMVVRVPPFL PILFLASHVGKSPSPSPHF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13725	27626	A	13892	166	1	LFSKIFWWLLPVIPALREAKVGELLEPGSSRPAAWATWKNPVYTKNTKISQAWQCT
13726	27627	A	13893	128	2	FSTYPNPFIKLPHPYLPPLTLFLDSAHLHPSEINSLVAQKKK
13727	27628	A	13894	225	391	HLSTHILTPFPFSLPEQWLVPIIPVLWEVKMGGLLEPRSSRPAAWATQDPQVSRK
13728	27629	A	13895	192	1	TLVCVSSSVPKYNNNICLACWFMPTIPA LWEVESGSLLELKSSPPAWPTWWVPLKS KNTKISLA
13729	27630	A	13896	152	245	DQSIADVLMYTHTHTHTHTHTHTHLQNVPG
13730	27631	A	13897	270	406	ISTRFFLYRDRASLCHPGWSAGVQSWLPGSSNSQAQAILLPQPPE
13731	27632	A	13898	232	73	EAEGPRDVTSSTFHWRLYDQTTNYHECRMWANSRLRLTPEGLLKVIPTWCHAH
13732	27633	A	13899	107	7	LGQAQWLMPTIPALWEAKAGGSLEPRTSRPAWA
13733	27634	A	13900	62	224	PTRPILAHCNLCVLGSDDPASASQSAGVTGMSHCAWSNLIHLPSRSTAICTL
13734	27635	A	13901	450	194	KRQVKSHSEVKTTHVQWPGIDPGSPAWEARILPLNHQRLSGTTPWRITEKSNHKDL ETVLSGFFKCRCLKANKDIQTKCVFIGNFY
13735	27636	A	13902	300	404	AAPGRAPQKKKKKKKKKKKKKKKKKKKAPFIKRGR
13736	27637	A	13903	131	29	ALGSLQPLSPRFKRFSCLSLPSSWNSTALTVTTM
13737	27638	A	13904	267	74	VWVLVPPFTSYGVLDKPIIVNNIYVHV CVCLCMCVVCVCCTVIRRHCHWHNMI I IISQHDQ
13738	27639	A	13905	193	64	IRSHQIHKLHFKKFRILGWTWWLTPVIPAPWEAEGRSPEPSS
13739	27640	A	13906	309	424	QSTDFLENRRRVGWAWLTPVIPALWEAEVGGLPEIKNS
13740	27641	A	13907	404	251	SCLISLRSDYRHHVPPQANFVFFFEM ESCSVAQSGVQWQEENSISKINK
13741	27642	A	13908	471	59	GPPQAKKGKGFPTPGPPQKGGGQPKSGVLGFSPPPLGCPGLGPPKGWGFWGGSF FFFFFFRKWEHKNELFPFSKTEKPRRAGEARKGSQSTKYAGLSRGERQASPTLRPGHLAKASAGGWLQYTRWQGLPEPGN
13742	27643	A	13909	479	231	QBYCMLIFCEHFGDFDLNIVFCLEKMKVGVIAIFYLLSSFTGRPQWLMPVIPTLWEAEVGSLEAKSFTPAWATWQDPISMF
13743	27644	A	13910	167	19	CIVLGIMLDSLWEPRQWVPSVWRWFTPVIPALWEAEAGGSPEVRSSNSS
13744	27645	A	13911	328	446	GSFSKITDLSQTWWYVPVIALQSEVGRSLEPRSSRLQ
13745	27646	A	13912	145	460	NAFMSTGCEVLSYSELQRNLVWVWFLPVIPATPQAEAGRLGPRSSRPWATKGVRALSHKQNTNTKTKLSHSTGVSVFTHHIHSPGILWRLSQWLLAMNLATN
13746	27647	A	13913	319	210	KLGFEEKGPPLFFFFFFFFFFFFFFFFGFLTVSCNFTL
13747	27648	A	13914	372	10	PNTTCTPITYGKKCCPREISYYLCHEFTIRIRILTFDGEDSCYIAQAGLKLGRSPPTSASGVAGNTDVCHHTQPIIFYILETG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LALLPRLILNSWSQAILLPQPLRSYFNFWLFFCLYN
13748	27649	A	13915	594	471	PSYIAYMCICMCVCVYVYINICVCIYTHVHTPYNPVISKN
13749	27650	A	13916	235	3	EANNLIRKTYTSGWFQRTSKRPPAVRRMKVLFFETESCSVAPVGVVHDSLLQPRPPGLNRSSHLSPSSSDYRWA
13750	27651	A	13917	272	184	KTTAWAQWLTPTVISTLWEAKVGGSLAEGS
13751	27652	A	13918	46	321	SRVQGTGGHRGRGCTIAGVGEQEAQRET EGPPWRWLTPVISKLWEAKAGGSLEPVS SRRATWNLLKRIYYTDREYLIPLALNT SQGSTFSF
13752	27653	A	13919	387	484	FIEIIGWARWLMPTVPTLWEAEAGGSPEVRSS
13753	27654	A	13920	142	321	FLFSIHFLSCWGLFSNVQSLSIFS KVRLYGQAWWFTPIILALWEDKAGGSLD PRSL
13754	27655	A	13921	270	412	IEDKKIYSILHTETLERQARWLTPVIPAFWEVKAGGSFEPRLRPV
13755	27656	A	13922	304	396	NFGWAQWLTPTVIPALWESEAGGSLEPRGLRS
13756	27657	A	13923	305	387	VWWTPTVIPALWEAEAGGSPEPRSSRP
13757	27658	A	13924	103	3	NKSPELGWAWLAPVIPALWEAEAGGSP EVRSS
13758	27659	A	13925	195	400	CLLILSGLVASCIIERHGKGQAWWLMPTVPTLWEAKVGGSLRLNRLRS AWGTWRNS ISIKYTEQLAQG
13759	27660	A	13926	294	489	KWAKMQTLHKGRYACVCICVCVCVYTYTDIYIFYIHIWPMNTKCSMLLVIGEMKILSRMWSNQ
13760	27661	A	13927	363	2	NWGPPGFPPPPFLKTGPVFFIFGAPKKK FELSTPRALKFVLLKGGPLFFFFFLWV FLVKTGSHCVAQPDLELLSSNPVLVSQ GAGITGMSPQVQPLDLFFFSFFETGSR SYAWADAW
13761	27662	A	13928	1	218	LRFKKRKTNPKPMWSVHTMEYHSALKRK BIRTQTTRWINLEDIVLSEIRVAVTKGR ILYDSTQMRNLEESNL
13762	27663	A	13929	219	408	TFCHFIAFLHVKMFVVFVFFSFIMFFFP LNCNKAERKKKKKNNKKKKKKRKKIS LSPPAPP
13763	27664	A	13930	161	22	WHPPASASHVAGTTGACHHERLRQEDHF SLRVQGCSEPRLCCHHTPP
13764	27665	A	13931	116	1	INTGWARWLTPVIPAFWEAAVGGSLPR STSQAATWK
13765	27666	A	13932	181	38	PWPQRATQPKISPLPPAISALWEAEAGG ALEPRSSRPAAKSDAWVD
13766	27667	A	13933	267	397	TVFDRTLFFIKKIHSWAPWLTPVVPAL WEAEVCGSPEVRSSG
13767	27668	A	13934	129	12	NIGVGWALWLTSPVLPALWEAEAGGPPKV RSSRTARPMS
13768	27669	A	13935	179	1	KTYYGGIPPGPPKKGEKKPPFFFKKFF LFFISFFIFFFFFFLRLQSLAKMQSASVW KVS
13769	27670	A	13936	245	616	DDKKKKEAAQKKATEQKIKVPEQIKPSV SQFPANSNNGTSTATSTNNNAKRATAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NQQPQQQQQQQQPQQQQPQQQPQPQPQQ QQPQQQPQALPRYPREVPPRFRHQEHKQ LLKRGQHFPEF
13770	27671	A	13937	121	292	NTDLDLALALIVRVLTSDDNFKNWGWVQ WLMFPVFPAPWEAEVGSSEATNLRPAWA T
13771	27672	A	13938	421	202	GPREAPLFPSTQGISRPLFFFFFETES RTVTRAAQWHNLGSPQPPLCSLDILKT SQSVCMPAEAILVSQIT
13772	27673	A	13939	205	543	ILESRRRLGWSEALPENQLLCRASSWES LGPDPPCLKPPSPAFWGAAGGWRAKST SVSEPVVGTLLVALFLEMAVGLLLGLP FCFHSLGAPHLCEPDGPSVLPAEARQS R
13773	27674	A	13940	140	2	LSQHSEETLPPPLYLEKESRRPPPPQH TPHPPPPWPWHPDIADIQ
13774	27675	A	13941	47	303	GLIFLIITWTCIVKTSTDFPRMEDCSQCI HQVTEESNKRMGFLSYIANPHHGSSRL WPQHAAPWDDGRRGKPVFSLGFVSFPFP Q
13775	27676	A	13942	1488	1719	PLVSFSKNTYPCLGNVKNQKTTFCRSRW KLHVLSSNLSSPAEVTVASINLVVSEQ SFQNSQLPAMLCILVHLQMS
13776	27677	A	13943	127	402	QVTHPPNRTMCSSMIFFLYLCLFLSL PFPSHLSLYAPPKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKAGGGGPFK KKIHFPGGGRIIFY
13777	27678	A	13944	852	209	EQTVYCTRIDLQOKLVFLRLFAFCLLSQ GDPGSPMMCQLQQFDLWVLRGVNFGGE TCPGLFLYTKVEDYSKWITSKAERAGPP LSSLHHWEKLISFSHHGNATMTQKTY DSELGHVGSYLQQRRTITHSRLGNSSR DSL DVREKDVKESGRSPASVQPLYDY YGGVEVGEGRIFAGQNRLYQPEEILGSL RACFLFAAVSSPGATPPN
13778	27679	A	13945	68	260	INIFWHCVLLYVILYAISQFLFPCKVN IASWLGSAHACNPSTLGGQAGESLEPR NLRPAWAT
13779	27680	A	13946	420	156	FLPPGVKYGSFKRAPPPPPPPFLVET LSCYIAHTGLELPDSSNYPTSASQSAVI TGMSHHTWPLEGACLAIPQALRILLVLV PLH
13780	27681	A	13947	317	17	AGHGGSTCNPSQPIVTAVPINLWGRDLL QQWGAQAFIPEQLYSPQSQHTMQEMGYV PGMGLEKNLKGKLPQAEQGNSHQGLG YNFSWQPLLSLQNLYL
13781	27682	A	13948	55	224	NFRLTSSFSYLKMSFWLGMWLTVPVIAL WEAKTGGLFEARSRLRVWVQSKKAGSHL
13782	27683	A	13949	1464	805	RATSVRGAGRERSCGAAWSPASIGPFLR RSVLPNAHFRSSREGGMAASTDMAGLEE SFRKFAIHGDPKASGQEMNGKNWAKLCK DCKVADGKSVTGTVDIVFSKVKGKSAR VINYEFPKALEELATKRFKGSKEEAF DAICQLVAGKEPANVGVTAKTGGAVDR LTDTSRYTGSHKERFDESGKGKGIAGRQ DILDDSGYVSAYKNAGTYDAKVKK
13783	27684	A	13950	356	98	NAGPGIYFWGPICKTLPCPPAGVKLGSL KRAPLFFFFVEMGFHHVAQAGLKLSSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DSPIPVQSQIRITSTCEPPCLAKIKSSLRL
13784	27685	A	13951	194	48	NFLEGWPGQRLTPVIPALWKAEEAGGSLEPKTFRPVWAMWRDRLRKPQH
13785	27686	A	13952	341	418	DQPGQHGETPSILKIQKLAGRGSTCL
13786	27687	A	13953	158	323	TWLKKYFQSTNQLPPAHLNVPQLLPFGLELLPLKKKKKKKKKKKKKKKKKKKK
13787	27688	A	13954	231	355	VFLPQKQKQNCPLTGKWNNSWNHITLEYYSAVKGMKQLI
13788	27689	A	13955	493	39	PAAFSSWGWPSSLLKKTTPASWPPGLLEPAPVSSMAAPDLDSEFLPLCWTFRLVLCRVFSSSTLAFLSCVSTSFALTTPAASNIFSIISLPHWASPPLPTARLTSVSPPELPLPLPSRLQRPGRGAPSHPGMSMGPIILDATSNSTTSR
13789	27690	A	13956	497	372	NTKISWASWYAPVIPATWEVSNRPQAIHSHQPPKRIGLQA
13790	27691	A	13957	438	301	GTTYLDIDMTCDYVSVCLCIYICTRQQSYYITYVYTHTHTHMYI
13791	27692	A	13958	84	466	QPLGRSGKVPQLHLWEMQRLPAAFFRSFAAQGLGESVHINTPTSLSLRGRPFISSSGPGARARVTCAPCLHAARILCCFWRLHRLKCSNVISAHCNLRFSGSSDSPASASQVAGITGRSSLEQLLE
13792	27693	A	13959	216	28	KYVKNYVLSSIFWMQEIFHNFKKSSRTQWLTPVIPALWEAEAGGSPEPRSSRPASSIQLENS
13793	27694	A	13960	320	943	VLSFSLSDRAQRNCNRMGKQNSKLAPDEVMDLVKSTEFNEHELKQWYKGLKDCPSGRNLNEEFQQLYVKFFPYGDASKFAQHAFTFDKNGDGTIDFREICALSITSRGSFEQKLNWAFNMYDLGDGKITRVEMLIEAIYKMGVTVIMMKMNEGLTPEQRVDKIFSKMDKNKDDQITLDEFKEAAKSDPSIVLLQLCQDIQK
13794	27695	A	13961	191	8	GLFRFRRLSEEVKHCCCCCCCCCCCCCCCCCCCCCCCCCYLRLAPQSPAAPAPELHTPLPGSRNR
13795	27696	A	13962	203	28	VWGNQHFVFPVFRKKVFCFFPLNKLRLGGGFFFFFFFFFLVFIDNSWVFLGEGDLAAGS
13796	27697	A	13963	18	171	GIRHEERERERERERERERERERERERH PAREIDMCVSKRDTRGALCALF
13797	27698	A	13964	25	299	HDFCTRRERERERERERERERERERERE RERERERERERERERERERERERE RERERERERERERERETHLSLYIMCV FLYIPLYFSFLYIHTQREAPPPLSATLS LSIL
13798	27699	A	13965	246	410	AYNGQSGRGVTPVIPSLWEAKTGGSLERP RSWRSAWATWHTPPVPGPSKEISLYI
13799	27700	A	13966	91	26	FCCCGCCCCCFYCKEKTIV
13800	27701	A	13967	158	24	PFCHIIYIFLESCFVAMLECSGKILAH YLRLLGSSNSLVPSLA
13801	27702	A	13968	129	7	SWAQWLMPITLWEHEAGRSLEAMSSR PAWATQQDPVSKK
13802	27703	A	13969	445	268	KIQLTKLKNASESLPSRINQAEKISGW AWCLMPVIPVLWEAKAGGSLEPRSLRRG QVT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13803	27704	A	13970	1628	1309	HRRKKCAGYSSLSSALLRERERERERER ERERESVVCVCLGTITCFRRQYCVIQGI SGVRQNCVQIPALSDPDLFLFLSLSVLH SNTWVVPRPTLRVERTERNKGAMCV
13804	27705	A	13971	314	140	QCHNCYILTQLVKIKGDAQAWLMPIIPA LGAKAGGSLEAGSLRSAWATWRAPMSTK IF
13805	27706	A	13972	292	482	YKSVRTQDSCAHGVDRLVGKIRYVNLFV YICQHSDGRTWWLTVPVIPPLWETKGGGS SEVGSRSG
13806	27707	A	13973	502	303	STAIGPSFSFPFLCTHGSHFGFLFFFFCF CFFFLVEMGSHYVAPAGLKLLGSSDDPPAS ASPShLGLQV
13807	27708	A	13974	493	289	IPPTALGTSSPFLCTHGSHFGFLFFFF CFCFFLVEMGSHYVAPAGLKLLGSSDDPP ASASPShLGLQV
13808	27709	A	13975	405	121	IREAAQSESILFVRAAPHTGLISGPCITE IYAVKDTRCMQRRIILVRELECAAHGLTE CLSIDTHTHTHTHTHTHTHTHTHTHTH HGTRWEAQSQLKGES
13809	27710	A	13976	135	254	TVTCTNSSWSLTFTSFFLMPGWIOKGR RVCVCVCVCVC
13810	27711	A	13977	179	58	VPLSINSPQRQCIFCCCCCCCCFLVLQ KIISERSWAEIG
13811	27712	A	13978	97	186	KTIIFWLGVVAHCNPSTLGGQGGRIMRG RD
13812	27713	A	13979	289	420	ELGLKIHGFPSQAPWFMPIIPALWEAEA GGLLESRSSRIAWAMW
13813	27714	A	13980	421	106	SGGRNFFFFFFLGGGFYKKKFPPPPFLRGK KKKPPLPKKNKNTPIFFPPGGGPPPFSP PKKGGGKIFFFFGGKNFIMQNFGGFPPL WGKKKKFLPKKNPLFFFFFF
13814	27715	A	13981	309	135	KHIYIYLSIYLSIYLSIYLSIYLPAAYLP TYLHAHPLIHANAYKNIHIDYPFKKGFE Y
13815	27716	A	13982	231	21	QHMYCLKSIWHKKLSRKPYCYIISEYSS MVKLRSVISQVQWLMFPVIALWEAKAGG LLKARSSRPMAI
13816	27717	A	13983	209	359	HLHTHTHTTPNGVKQIMTQIPILPLTG PLILEKFLNFSKPLSHPGKRDP
13817	27718	A	13984	391	249	IWPILPPQKIFFFFETESCSTQARVQ WCNLGSLQPPNPVFPSLAK
13818	27719	A	13985	181	403	YLVLDSPASTLGLSQPKDYITKDQTLT FRPVVVAHCNPSTLGSQKWITSVQEV ETSLCNTARPCLYQKYKN
13819	27720	A	13986	441	358	ETGSRCVILAGAQRDLSSVQPLPPRFK
13820	27721	A	13987	7	233	ASIPCITYQKTkipntkqtknkntkitpa wwctpiapatqkaeipplhssslgdflrl spkkkkggpnwaptpskff
13821	27722	A	13988	152	44	pkapLFFFFFFFFFYETRSHSVAQAKV QRHDHGSL
13822	27723	A	13989	188	379	NVSCHAAETRVWWEKERPLVPFPGAYLL DGMPLVWLLSASSILSIWLSIYLSIYLS IYLSIYF
13823	27724	A	13991	296	53	SSI LFHASKYHFSGRLFSLLSCKRRNII QLVPHMYSPLYMIYITHTKHIYEYMHVH IYIYMNLNRNCRIYLSHCKTPKENQAR
13824	27725	A	13992	37	290	RLGSPASRHQQIQCLIRACLKDGTLGWV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WWLIPVIPALWEAKVGGSLPRSSTPAW ATQGDLLKKDGTLLQCPHVAKGHSSHS
13825	27726	A	13993	189	370	SRNAIFKKRWESSCQSSFNLSGVFPQAA TKGWVRWLTLPALWEAKAGGSLPRSS SRPA
13826	27727	A	13994	179	25	SKHNKKNIQICLLCSKRSMFVHVCIIHI ICVYVYRYAYIYIGMCIHIYIHS
13827	27728	A	13995	159	2	EDPLSPGVQDQHGHRKSLSGRGKISL GQEFKSSMAAMYFGRSGGCKLERR
13828	27729	A	13996	307	99	FIWEHFVNYTMFFTYKKPTSQANWLMV VPALWETEAGGSPEVSRPPGQHDDVR PLGPSLHVYLQMD
13829	27730	A	13997	218	21	FQHFGRPRRVDHLSLGVQDQPGQHGETP SPLASSILDLI PPPFIDE PVDLAFQSV TLGVQDTTS
13830	27731	A	13998	227	404	GYSVTLLGLTQLTQRIAHGTRKGERER ERERERERERVCSCLMHELASHLLFFFL FRE
13831	27732	A	13999	400	668	PVGRRWELQGMGLGVRTWQSSLPCCGPT SSSVLSLGRGTPGISNTCLPPRSATELG LPAQVPFPNVQSQDQDLSFSLGCFPTY NRQTL
13832	27733	A	14000	225	414	NRVLLCHTGWSTVAILAYCSFKLLGSRD SPTLASRAARTIVKCRNVWLIIKKKKKK KGGRRLL
13833	27734	A	14001	397	118	LFSGPFFFDKSECFQEPVFFCLLLYNQ MQPYLLRSFAVDSYYMDSFLDRVVSFC QSGWSTVAPSRLTAALNSLAQVILLPQP LNVLCGISR
13834	27735	A	14002	3	173	YVFYRQKQMVCFYKIRIKNMFNRRLNL GQWCVPV PATQVAEAGGSPEPTSLRPI
13835	27736	A	14003	440	290	YHTLYIYIYIHTHTHTYIYLCTYWG QFDLLVLDNKLYKEIYLSVFI
13836	27737	A	14004	2	116	ARLVAMPFKYEETKDFLLTARRKDAKSV KIKKNKSAAV
13837	27738	A	14005	279	422	SAKAPLSCLRTNSLLKNGLRGWAWWIT PVIPTLWEAEVGGSPDVTSP
13838	27739	A	14006	3	497	GGIGDSRCGSTRASSPQLAGRSSSVLP AAQPCPTPMDVFKKGFSIAKEGVVGAV EKTQGVTEAAEKTKEGVMYVGAKTKEN VVQSVTSVAEKTKEQANAVSEAVSSVN TVATKTVEEAENIAVTSGVVRKEDLRPS APQGEASKEKEEVAEEAQSGGD
13839	27740	A	14007	1	292	SLGGGGCNDPRSYHCTPAWATEQDTSV SLSIYMSVRVCIYMYMCVCVCIRIYTYI HTHIHIRVYIYTIPIYIYIYIYVDLV IYMGWCGCPPPSI
13840	27741	A	14008	57	250	KIFFFLMNTWGGVPVVLATWEAEVGG LEPRSLQETMMTSLLSRLPRQGEIL SLILKRN
13841	27742	A	14009	184	2	AVPGRWPCQVPGLLPSIQDTLKQGRGT QWLTPVTPMPWEAEAGGSLDARSLRPAW ATGK
13842	27743	A	14010	123	3	KEPSRPGRWLTSTIIPACWEAEAGGPPEA RSSTREFRTAK
13843	27744	A	14011	403	168	GTGLRASRCISQPVMSGLLSPSEFPFPE IESHLHVSQRETAARLDRERERARERE RERERGNASSGKPPGSASCVP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13844	27745	A	14012	207	422	EIRRGSLAGPLSLNFTLSVMGSHSKYLRLKVGRAQWLMPPVVPALWEAEVGLHBLRLGHTWAAW
13845	27746	A	14013	200	405	WLCVLGWSLLALSPLRECYGPTSAHCNLLLRSSDSPASASQALQEAQYQHLLMM PQAASTQVGRKK
13846	27747	A	14014	319	176	KPSTITFLFLHLFISSRESRPVTQTEVKWLNHSSPQPPTPRFSLPSS
13847	27748	A	14015	63	401	EQENKNTLNSPGWDGVHIVLRFNTRMPLGHLSEFSEGVSGSGSRRQAGAGGRSATAAARPCQCLGLKGLPPAVPSCGLEG KAPERAGYSASHPHGCETGNGWVLYVN
13848	27749	A	14016	416	63	VSKVYPKINHRTQRTVRHETFKIAMPKYYSNLCSILRFNDRALAFMRHYTKQCSRTS ITEYIAMFFVCLFVLKIGAHCHPGWNE VVLVCSQVTAASTSRAQAILPPQPPKIL GMQQA
13849	27750	A	14017	196	425	SLMFRPPLFSFCCFCIRYPIFVFFSLLCFASFWSCLLFFFFHYLKLFLLLFLLFF LPVLLCLDSFLVHDFLLSS
13850	27751	A	14018	3	233	SSRMGRGKTIAFDMRWSCEVDRARHRDREREREREREREREKGAEPQEFVISPW VDRPCLAGILHLKCGCGHRL
13851	27752	A	14019	163	1	AERWHDQICVEREIWGWQWLMPIVPLWEAKAKNLEPKNLKLQRNRRPGNSR
13852	27753	A	14020	203	83	LKKKKKNKSQAQWLTSSVVLASQEAEGGSLEPRNSRPAAWAT
13853	27754	A	14021	179	3	VTWQRELRLQMELRLLICRAWLTPVIPVPWEAKAGGSPEPRSSRPAAWETRNRPGNS
13854	27755	A	14022	358	431	WHKKKNQNLGTGAHACNPSTLGG
13855	27756	A	14023	98	3	GRPAGWLTTPVAPTLLWEAEMGGSLEPRSLGHE
13856	27757	A	14024	254	385	RENWAEPPSSHSLNIFLQLGTVARACNPSTLGGRGWITRSGD
13857	27758	A	14025	140	1	KGVLDPGRGLCVFCFFFLCVCVCVCVCVCVWRSLTSLPRLQCI
13858	27759	A	14026	579	852	QREWVGWAGKEGEGWVSHVPASQALPAN GQRGQPHPSPLGGTGSTWAQEGAYCCLS SCSHCCCCSSCCCCPPGFCLFPLGAI CHLYHL
13859	27760	A	14027	30	663	LRIRALRELPAHIPGSLTICVPRPPLPCSSSTKPDAGYKPLAQKLGSRGTGPC LGHAPCYSPLWELRGHGCSPYGSPSGS VSLWQEAAMRLPKNTPBEKDRRTAALQEG LRRAVSVPLTLAETVASLWPALQELARGNLACRSDLQVAAKALEMGVGFAYFNVL INLRDITDEAFKDQIHHRVSSLLQEAKT QAAVLVDCLETRQE
13860	27761	A	14028	1	267	AVGVHHAFLPHCFASLLESPVSPRLA MDPNCSCAAGVSCTCAGSCKCKECKCTSCSKSCSCCPVGCCKAQCVCCKGASEK CSCCD
13861	27762	A	14029	46	1746	PAAGAATMEFRQEEFRKLALGKLRHRLLEKROEGAETLELSADGRPVTTQTRDP PVVDCTCFGLPRRYIIAIMSGLGFCISF GIRCNLGVAIVSMVNNSTHRRGHVVVQ KAQFSWDPETVGLIHGSFFWGYIVTQIP



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						GGFICQKFAANRVFGFAIVATSTLNMLI PSAARVHYGCVIFVRILQGLVEGVITYPA CHGIWSKWAPPLERSRLATTAFCGSYAG AVVAMPLAGVLVQYSGWSSVFYVYGSFG IFWYLFWLLVSYESPALHPSISEEERKY IEDAIGESAKLMNPLTKFSTPWRFFTS MPVYAIIVANFCRSWTFYLLISQPAYF EEVFGFEISKVGLVSALPHLVMITIVPI GGQIADFLSRIMSTTNVRKLMNCGGF GMEATLLLVGYSHSKGVAISFLVLAVG FSGFAISGFNVNHLDIAPRYASILMGIS NGVGTLSGMVCPPIVGMATKHKTREEWQ YVFLIASLVHYGGVIFYGVFASGEKQPW AEPEEMSEEEKCGFVGHDQLAGSDDSEME DEAEPPGAPPAPPSPSYGATHSTFQPPRP PPPVRDY
13862	27763	A	14030	240	63	VFTAQSNNGVELNRFNEGPLSAVLKGRV AWAQWLTPIPTLWEVKAGGLLEARSLS PA
13863	27764	A	14031	289	414	HAEMGRVQWLTPAIPALCKAEAGGPPEP RSLRPAWATY
13864	27765	A	14032	386	1765	LG DARAPEKMSAIQAAWPSGTECIAKYN FHGTAEQDLFPCKGDVLTIVAVTKDPNW YKAKNKVGREGIIPANYVQKREGVKAGT KLSLMPWFHGKITREQAERLLYPPEGL FLVRESTNYPGDYTLVCSDGKVEHYRI MYHASKLSIDEEVYFENLMQLVEHYTSD ADGLCTRLIKPKVMEGTVAQADEFYRSG WALNMKELKLLQTIGKGEFGDVMLGDYR GNKVAVKCIKNATAQAFLAEASVMTQL RHSNLVQLLGVIVEEKGGLYIVTEYMAK GSLVDYLRSGRSVLGGDCLLKFSLDVC EAMEYLEGNNFVHRDLARNVLVSEDNV AKVSDFGLTKEASSTQDTGKLPVKWTAP EALREKKFSTKSDVWSFGILLWEIYSFG RVYPYPRIPKDVVPRVEKGYKMDAPDGC PPAVYEVKNCWHLDAAMRPSFLQLREQ LEHIKTHELHL
13865	27766	A	14033	619	414	EQARCLEQHACTSPRQPRQLQCSELKG HSLGMEHQGHVPCLHPCSPCPPVKASPA CWSSNPAPLCPH
13866	27767	A	14034	2	614	LESRPDGRPSSTHPASPSAFSAPGKPHP PEAKMSSKRAKAKTTKKRPQRATSNVFA MFDQSQIQEFKEAFNMIDQNRDGFIDKE DLHDMLASLGKNPTDEYLEGMMSEAPGP INFTMFLTMFGEKLNQTPEDVIRNAFA CFDEEASGFIEDHLRELLTTMGDRFTD EEVDEMYREAPIDKKNFNHYVEFTRILK HGAKDKDD
13867	27768	A	14035	1	254	AVEFGPAGPGSLGRAAAMIIPVRCFTCG KIVGNKWEAYLGLLQAEYTEGDALDALG LKRYCCRRMLLAHVDLIEKLLNYAPLEK
13868	27769	A	14036	494	148	FRFLSDCGVFAEGHIELQVESGVPLGFS TMAEDMETKIKNYKTAPFDSRFPNQQT RNCWQNYLDFHRCQKAMTAKGGDISVCE WYQRVYQSLCPTSWTWDWEQRAEGTFP GKI
13869	27770	A	14037	130	3969	IMGDVKNFLYAWCGKRKMTPSYEIRAVG

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						NKNRQKFMCEVQVEGYNTGMGNSTNKK DAQSNAAARDFVNYLVRLINEIKSEEVPAF GVASPPPLTDTPTTANAEGDLPTTMGG PLPPHLALKAENNSEVGASGYGVPGETW DRGANLKDYYSRKEEQEVQATLESEEVD LNAGLHGNWTLNNAKARLNQYFQKEKIQ GEYKYTVQVGDHNRSFIAEMTIYIKQLG RRIFAREHGSNNKLLAAQSCALSLVRQLY HLGVEAYSGLTKKKEGETVEPYKVNLS QDLEHQLQNLIIQELNLEILPPPEPSVP VALNIGKLAQFEPSQRQNVGVVPSPP QSNWNPWTSNIDEGPLAFATPEQISMD LKNELMYQLEQDHDQLAILQERELLPVK KFESEILEAISQNSVVIIRGATGCGKTT QVPQFILDDFIQNDRAAECNIVVTQPRR ISAVSVAERVAERGERGEPGKSCGYSVRF ESVLPRPHASIMFCTVGLLRKLEAGIR GISHVIVDEIHERDINTSFLLVLRDVV QAYPEVRIVFMSATIDTSMFCEYFNCP SLKLWRTYPVQBYFLEDCTQMTFVPPP KDKKKKDDDDGGEDDANCNLCGDEY GPETRLSMSQLNEKETPFELIEALLKYI ETLNVPGAVLVFLPGWNLIYTMQKHLE NPHFGSHRYQILPLHSQIPREEQRKVFD PVPVGVTKVILSTNIAETSITINDVVYV IDSCQKQVKLFTAHNNMNYSTVWASKT NLEQRKGRAGRSTAGFCFHLCSRARFER LETHMTPEMFRTPLHEIALSIKLLRLGG IGQFLAKAIEPPPLDAVIEAHTLRELD ALDANDELTPGLRILAKLPIEPFRGKMM IMGCIFFYVGDIAICTIAAATCFPEPFVNE GKQLGYIHRNFAGNRFSDHVALLSVFQA WDDARMGGEAEIRFCEHKRLNMATLRM TWEAKVQLKEILINSFGPEDCLLTQVFT NTGPDNNLDVVISLLAFGVYPNVYHKE KRKILTTEGRNALIHKSSVNCPSQDM NYSPFFVFGEKIRTRAIKAGMTLVPP LQLLLFASKKVQSDGQIVLVDDWIKLQI SHEAAACITGLRAAMEALVVEVTKQPAI ISQLDPVNERMLNMIRQISEPSAAGINL MIGSTRYGDGPRPPKARYDNGSGYRRG GSSYSGGGYGGYSSGGYSGGGYGGSAT PSGRICAGVGGYRGVSRGGFRGNSGGD YRGPSGGYRGSGGFQRGGRGAYGTGYL DIEEEVAAIKLGYVSSVCRQ
13870	27771	A	14038	431	542	EGITPGWARWLTPTVPIGLWEEEAAGSGPG REIDIGLAN
13871	27772	A	14040	238	362	RRCTFLSFRMLAPRVYSVVGKRAFSPSV CVRAHGKCDYSYS
13872	27773	A	14041	6290	3514	FRAAGSSSTNSGRICPLPSGALLYQSEG LLARPHGKGSFQVGRQQHQAIVRVGSAHA SSAGYVCVSAPFPVFLRFCKVGGPGISR VYALFYGECNPTREWAVSSELSPSFQEQ NKMNKVEQKSQESVSFKDVTVGFTQEEW QHLDPSQRALYRDVMLENYSNLVSVGYC VHKPEVIFRLQQGEEPWKQEEBFPQSFS PEVWTADHLKERSQENQSKHLWEVVFIN NEMLTKEQGDVIGIPFNVDVSSFP SRKM

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						FCQCDSCGMSFNTVSELVISKINYLKK SDEFNACGKLLLNLIKDETHTREKNEVL KNRNTLSHRENTLQHEKIQTLHDNFEYS ICQETLLEKAVFNTRKRENAEENNC DYN EFGRTFCDSSSLLFHQISPSRDNHYEFS DCEKFLCVKSTLSKPHGVSMKHYDCGES GNNFRRLCLSHLQKGDGKGEKHFECNEC GKAFWEKSHLTRHQRVHTGQKPFQCNEC EKAFWDKSNLTKHQRSHTEGKPFECNEC GKAFSHKSALTTLHQRTHTGEKPYQCNAC GETFYQKSDLTKHQRHTHTGQKPYECYEC GKSFCMNSHLTVHQRTHTGEKPFECLEC GKSFCQKSHLTQHQRHTHIGDKPYECNAC GKTFYHKSVLTRHQIHTGLKPYECYEC GKTFCLKSDLTIHQRHTHTGEKPFACPEC GKFFSHKSTLSQHYRHTHTGEKPYECHEC GKIFYNKSYLTKHNRTHTGEKPYECNEC GKTFQCQSQTQHQRHTHIGEKPYECNEC GKAFCHKSA LIVHQRTHTQEKPYKNEC GKSFCVKSLIFHERKHTGEKPYECNEC GKFFRHKSSSLTVHHRHTGEKSCQCNEC GKIFYRKSELAQHQRSHTEGKPYECNTC RKTFQSQKSNLIVHQRHIGENLMNEMDI RNFQPPQVSLHNASEYSHCGESPDILNV Q
13873	27774	A	14043	187	422	LTIPKLHSAQEPAGPVSPPPPPSPTFQI GGRSRAEPRNQYCPQVAPVPALRGCLPL SPGEPPHDTSSPRHLTCGGIVF
13874	27775	A	14044	340	442	NKFLSWVRLIMPVIPTFWEAKVGGWLEA RSLRMQ
13875	27776	A	14045	3	1240	LVEGAAGQGVSDGARLRKCGTRSFPGSE EVLSSMARGSAFPAAALWLSILCLLA LRAEAGPPQEESSLYLWIDAHQARVLIGF EEDILIVSEGKMAFFTHDFRKAQQRMPA ISVNIHSMNFTWQAAGQAEYFYFSLR SLDKGIMADPTVNVPLLGTVPKASVVQ VGFPCLGKQDGVAAFEVDVIMNSEGNT ILQTPQNAIFFKTCQQAECPPGCRNGGF CNERRICECPDGFHGPHEKALCTPRCM NGGLCVTPGFCICPPGFGVNC DKANCS TTCFNGGTCFYPGKICPPGLEGEQCEI SKCPQPCRNGGKICGSKCKCSKGYQGD LCSKPVCEPGCAHGTCHPEPNKCQCQEG WHGRHCNKRYEASLIHALRPAGAQLRQH TPSLKKAERRDPPESENYIW
13876	27777	A	14046	18	274	YSQEVLCENMRSGVVSNIKRGWAWWQLT TTIPALWEAEVGGLEPRSLRLASPQPP QHEDYSMSYCAQPRFSLCIRGFIFYSLW F
13877	27778	A	14047	177	441	GGSHYAWNITFIETKLIAQFFCFFEMO SCSVARLECRGAISAHCNLHLPSSNSP VMAQILKNQRKSNFDEDATLLGLSYTLL GEI
13878	27779	A	14048	136	319	DVFLLLFHSNYFLFFETGSHSVSQAGVK WCDLSSLQPPPLGSSDPPTSASRVPALF FFLEF
13879	27780	A	14049	388	128	ELKLFPSYKGQSPQLSLRRYFADLTAIVS NRFTLCPSARHLAVYLLDLFMDRYDISI

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						QQHLHLVALSCLLLASKYESDLHDWKF LFI
13880	27781	A	14050	262	3	VIYNYISVRPFPNIYHTFYTTL SFLYLS THTHTHTHTHTHTHQRETHGVCVCIYTYM YMCMYAKWYKFTFLISGKARIHTHLHPCI
13881	27782	A	14051	149	423	YPHLC AFLLLPSISSFRAGVFFFSYLSL TAYPLTWKPPPEPATPQPTPNPPPGHPA TRGPKSALLDHSYACASAPPLGTEGTAP SPSFALI
13882	27783	A	14052	2	1440	FVAVTAMAAPCLLRQGRAGALKTMLQEA QVFRGLASTVSLSAESGKSEKGPQNSK KQSPPKNNVVEPKERGLLATQTAAELSK NLSSPSSYP PAVNKGKRVASPSPSGSVL FTDEGVPKFLSRKTLVEFPQKVLSPFRK QGSDSEARQVGRKVTSPSSSSSSSSSDS ESDDADVSEVTPRVVS KGRGGLRKPEA SHSFENRAFRVTVSAKEKTL LQKPHVDI TDPEKHPQPKKKGS PAKPSEGRENARPK TTPMRSQVDEEFLKQSLKEKQLQKTFRL NEIDKESQKPFVKGPLPVHTKSGLSAP PKGSPAPAVLAEEARAEQQLQASPPGAA EGHLEKPVPEPQRKAAPPLPRKETSGTQ GIEGHLKGGQAIVEDQIPPSNLETVPVE NNHGFHEKTAALKLEAEGEAMEDAAAPG NDRGGTQEPAPVPAEPFDNTTYKNLQHH DYSTYTFLDLNLLELSKFRMPQPSSGRES PRH
13883	27784	A	14053	177	1253	EKKRTL PVRSVT GELQGKSLSDLAAGTM DSEKKRFT EEEATKYFRERVSPVHLQILL TNNEAWKR FVTAAELPRDEADALYEALK KLRTYAAIED EYVQQKDEQFREWFLKEF PQVKRKIQES IEKLRALANGIEEVHRC TISNVSSSTGAASGIMSLAGLVLPFT AGTSLALTAAGVGLGAASAVTGITTSIV EHSYTSSAEAEASRLTATSIDRLKVFKE VMRDITPNLLSLLNNY EATQTIGSEIR AIRQARARARLPVTTWRISAGSGGQAE RTIAGTTRAVSRGARILSATTSGIFLALD VVNLVYESKHLHEGAKSASAEELRRQAQ ELEENLMELTQIYQRLNPFCHTH
13884	27785	A	14054	1585	2099	ICVKTFFPPLALQVRMAAAEHHSGLPY WPYLTAETLKNRMGHQPPPTQQHSITD NSLSLKT PSERLLYPLPPSAPPSADNLT KPPECLLTPLPPSALPSADDNLKTPAE CLLYPLPPSADDNLKTPPECLFTPLPPS APPSVDNLT KPPECVCSLPFHPQRMII SRN
13885	27786	A	14055	2	2865	ALPDGGASVASDRAEGRPAKPSKTAARE KTEGAVAAVGGGPSSFRCCYGCCHEARL GRTSLPRGVIML TEASLSIWGWGSLGIV LFLITFGPFVIFYLT FYILCFVGGGLVV TLLFGKTNSEKYLEQCEHSFLPPTSPGV PKCLEEMKREARTIKIDRRLTGANI IDE PLQQVIQFSLRDYVQYWYYT L SDDDESFL LEIROTLQNALIQFATRSKEIDWQPYFT TRIVDDFGTHLRVFRKAQQKITEKDDQV KGTAEDLVDTFFFEVVEVEKEVCRLVC

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						TSPKDEEGFLRDLCEVLLYLLLPFGDFQ NKIMRYFVREILARGILLPLINQLSDPD YINQYVIWMIRDSNCNYEAFMNI IKLSD NIGELEAVRDKAAEELQYLRSLDTAGDD INTIKNQINSLLFVKVCDSRIQRLQSG KEINTVKLAANFGKLCCTVPLDSILVDNV ALQFFMDYMQQTGGQAHFFWMTVEGYR VTAQQQLEVLRSRQRDGKHQTNQTKGLL RAAAVGIIYEYQLSEKASPRVTVDYDLVA KLADTLNHEDPTPEIFDDIQRKVYELML RDERFYPSFRQNALYVRMLAELDMKDP SFRGSDDGSGESFNGSPTGSINLSLDDL SNVSSDDSVQLHAYISDTVYADYDPYAV AGVCNDHGKTYALYAITVHRRNLNSEEM WKTYRRYSDFHDFHMRITTEQFESLSIL KLPEKKTFFNMMDRDFLEKRRKDLNAYLQ LLLAPEMMKASPALAHYVYDFLENKAYS KGKGDFAKMDTFVNPLRNSMRNVSNV KSLPDSLAEGMTKMSDNMGKMSERLQD IKQSFFKVPPLIPKTDSDPEHRRVSAQL DDNVDDNIPLRVMLLLMDEVFDLKERNQ WLRNRNIKNLQQLIRATYQGTINRKIVD HVDWMTSPEQVADSVKFRDAFWPNGIL AEAVPCRDKSIRMRTRVAGKTKLLAIMP GE
13886	27787	A	14057	311	150	FLCFKYRRGFATLHSGKLKLGSSDPPSS TSQIPGITGTSHCVQPTHLFFLALS
13887	27788	A	14058	53	211	RQHITCLDIFFIHMNYKYKYNITYLSIY LSIYLSIYLYLSISHSYITERA
13888	27789	A	14059	1	1642	RDGRKMATATIALQVNGQQGGGSEPA AAVVAAGDKWKPPQGTDSIKMENGQSTA AKLGLPPLTPEQQEALQKAKKYAMEQSI KSVLVKQTIHQQQQLTNLQMAAQRORA LAIMCRVYVGSIIYELGEDTIRQAFAPF GPIKSIDMSWDSVTMKHKGFAFVEYEV EAAQLALEQMNSVMLGGRNIKVGRPSNI GQAQPIIDQLAEARAFNRIYVASVHQD LSDDDIKSVEFAFGKIKSCTLARDPTTG KHKGYGFIYEKAQSSQDAVSSMNLFDL GGQYLRVGKAVTPPMPLLTPTATPGGLPP AAAVAAAAATAKITAQEAVAGAAVLGTL GTPGLVSPALTLAQPLGTLTPQAVMAAQA PGVITGVTARPPIPTVTPSVGVVNPIL ASPPTLGLLEPKKEKEEELFPESERPE MLSEQEHMSISGSSARHMVMQKLLRKQE STVMVLRNMVDPKIDDDLEGEVTEECG KFGAVNRVIIYQEKQGEEDAEIIVKIF VEFSIASETHKAIQALNGRWFAGRKVVA EVYDQERFDNSDLA
13889	27790	A	14060	1238	1474	VLALQEGRPWRREPASIDACRLNFQRLR RGKFSNVLFPGLAQEALYSGGYHLKFAD ELMGCNLKKSTADASGSRGHQL
13890	27791	A	14061	266	400	GQWARPVIPALWEAKAGGSLEPSMLRPA GQHIKTPSVLITSKKT
13891	27792	A	14062	2178	1881	VLQAPSTILLAPRTDGGDMGRAMVARLG LWLLLLALLLPTQIYSETTTGTSSNSS QSTNTGLAPNPTNATTKAAGGALQSTA SLFVVSLSLLHLYS

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13892	27793	A	14063	261	1	NSVLTLLALLFSLHVLPPPPSGVTDTAG ALSTGGPPSPSTSVTGRGPAHSHASQLPP APGEFAPLNESCRGWAGEAFLEFRPD AWVDP
13893	27794	A	14064	2384	1115	QHFSRRGLCVVEQRSSVTSSWTS GAWSPPCPPSNASCNTLHTRD WASPDPGGQGS LGESPGP APPQGLHTLDTLHSLAQIGGK SPVAGVGNNGSLWPRES PGTANGHSPEHTPPGPGPPG PCPTKRRLPAGEADPVSS EEEGPAPRRRRGSLGHPTA ANSSDAKATPFWSHLLPG PKPVLDPDTCGPMGRRLK GARRLKLSPRLSLRKGPGL LSPPRASPVPTPAVSRLLG NFEESSLRGRFAPSGHI EGFTAIEIGASGSYCPQHV TLPVTVTFFDVSEONAPAF FLGIVDLNPLGRKGYV PKVGTIVQVTLFNPNTV VKMFLVTFDFSDMPAAH MTFLRHRLFLVPVGEEG NANPTHRLLCYLLHLFR SSRSRGRSLHGDIRLLF SRRSLELDTGLPYELQAV TEAPHNPRYSPLP
13894	27795	A	14065	232	416	GWAVQLGIGTEGKEGTSS SERQREGRGDGNRKTGR RRREGRRSTKTDAPSPY PAHRPRSKLI
13895	27796	A	14067	238	45	IQTGSHSFCIPSIWEAKAG LLEPRSLSPACPTQKDP ISHLGSEL PQSFRLLIRL VPLFLSAC
13896	27797	A	14068	3	1705	SCESKATPWRAVSASQELQ HPQGGQRSP LPGDLTPAR PNPAYPLTVEQRCSCSRPV PAPLPPHTHPPGSSCFYSS FSFITKATAPGAQRRAVTQ AERGRMGLGTGTWILVL VLPPIQAFPKPGGSQDKSL HNRLESAERP LNEQIAEA EEDKIKKTYPPENKPGQSN YSFVDNLNLLKAITEKEK IEKERQSIRSS PLDNKLN VEDVDSTKNRKLIDDYD STKSGLDHKKFQDDPDGL HQLDGTPLTAEDIVH KIAARIYEENDRAVFDKIV SKLLNLGLITESQAHTLE DEVAEVLQKLISKEANN YEEDPNKPTSWTENQAGK IPEKVTMAAIQDGLAKG ENDETVSNTLTLTNGLE RRRTKTYSEDNFEELQY FPN FYALLKSIDSEKEA KEKETLITIMKTLIDFV KMMVKYGTISP EEGVSY LENLDEMIALQTKNKLE KNATDNISKLFPAPEK SHEETDSTKEEAAKME KEYGSLKDSTKDDNSN PGGKTDEPKGKTEAY LEAIRKNIEWLKKHDK KGNKEDYDL SKMRD FINKQADAYVEKGIL DKEEAEAIKRIYSSL
13897	27798	A	14069	1	140	NTSVAIQTIEYSAFRRK ETLTHVPLWM NLKDTML REISQSQKDTV
13898	27799	A	14071	212	104	HTNHQCQT VLPAGQALAT PQGLAPSPVFPQSCLRMV
13899	27800	A	14072	358	112	FPLTVMLNVFLWWQNLK HFCWFIEQLM FFFFFL RTGSHYVQAGLELLGST NLPA SVSRVAGTTGIH NCTQFNPLHTLHL
13900	27801	A	14073	3	151	YMGFHHVGYAGLELLT SSDLPPWPPKCWDYR HEPSCLAMFFYFALIAPE
13901	27802	A	14074	8	1493	VTIHHLFVGVQAVRADT LKKKSPSCLLCTVFIP VPRIDL TNIDQVAVIF KHHFPVGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GDAVLK TWAPAQCLCSRMGPALWLGLT GILASVHCQPLLAHGDKSLQGPQPPRHQ LSEPAPAYHRITPTITNFALRLYKELAA DAPGNIFFSPVSI STLALLSLGAQANT SALILEGLGFNL TETPEADIHQGFRL HTLALPSPKLELKVGNLFLDKRLKPRQ HYLD SIKELYGAFAFSANFTDSVTGRQ INDYLRRQTYGQVVDCLPEFSQDTFMVL ANYIFFKAKWKHPFSRYQTQKQESFFVD ERTSLQVPMMHQKEMHRFLYDQDLACTV LQIEYRGNALALLVLPDPGKMKQVEAAL QPQTLRKWGQLLLPSLLDLHLPRFSISG TYNLEDILPQIGLTNINLEADFGVGTG QLNKTISKVSHKAMVDMSEKGTAGAAS GLLSQPPSLNTMSDPHAHFNRPFLLLW EVTTQSLFLGKVVPVAG

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-13901 , a mature protein coding portion of SEQ ID NO: 1-13901 , an active domain of SEQ ID NO: 1-13901 , and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively  
25 associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - 30 (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-13901.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.



13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-13901, a mature protein coding portion of SEQ ID NO: 1-13901, an active domain of SEQ ID NO: 1-13901, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-13901, under conditions sufficient to express the polypeptide in said cell; and
- b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 13902-27802, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NOS: 1-13901.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

5 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

10 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.